

adi gene. Homo
Lung cancer associ

ALIGNMENTS

RESULT 1
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ID AAQ46688 standard; cDNA to mRNA; 1611 BP.
XX
AC AAQ46688;
XX
DT 23-DEC-1993 (first entry)
XX
DE Human pp60 c-src gene.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Homo sapiens.
XX
PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US000445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn

Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-07-820-011A-3
; Sequence 3, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee/
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER, READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1611
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 20

PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-type Kinase
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-3

Query Match 99.9%; Score 1609.4; DB 1; Length 1611;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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us-09-44

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ID AAR39706 standard; Protein; 536 AA.

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AC AAR39706;

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DT 23-DEC-1993 (first entry)

XX

DE Human pp60 c-src protein.

XX

KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.

XX

OS Homo sapiens.

XX

PN W09314193-A.

XX

PD 22-JUL-1993.

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PF 05-JAN-1993; 93WO-US00445.

XX

PR 06-JAN-1992; 92US-0820011.

XX

PA (UYIA) UNIV YALE.

XX

PI Bell L, Luthringer DJ, Madri JA, Warren SL;

XX

DR WPI; 1993-243209/30.

DR

P-PSDB; AAR39705.

XX

PT Genetically engineered endothelial cells - which exhibit enhanced
cell migration, urokinase-type plasminogen activator activity,
and reduced mononuclear cell adhesion and fibronectin prodn

XX

PS Disclosure; Page 75-77; 91pp; English.

XX

CC The DNA encoding a portion or (more preferably) the entire pp60
c-src polypeptide (Given in AAQ46688) is used to transform endothelial
cells. Transformed cells produce increased amounts of pp60 c-src and
have improved therapeutic properties. They migrate at faster rates
than non-transformed counterparts; have an enhanced ability to
inhibit the formation of thrombi and/or dissolve thrombi once they
have formed and exhibit reduced mononuclear cell adhesion. They can
also be used to improve the success of surgical procedures such as
coronary angioplasty, heart bypass surgery, vessel graft and stent
implantation.

XX

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Length: 536

Ratio: 5.287

Gaps: 0

Percent Similarity: 100.000

Percent Identity: 100.000

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51 SerAlaAlaPheAlaProAlaAlaAlaGluProLysLeuPheGlyLys 67
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67 eAsnSerSerAspThrValThrSerProGlnArgAlaGlyProLeuAla 84
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401 ACATCCCGACGACACTACGTGGCGCCCTCCGACTCCATCCAGCTGAG 450
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301 LysProGlyThrMetSerProGlnAlaPheLeuGlnGlnAlaGlnVal 317
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seq_documentation_block:

; Sequence 4, Application US/07820011A
; Patent No. 5336615

; GENERAL INFORMATION:

; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration/
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 536 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: Linear

; MOLECULE TYPE: Protein

; HYPOTHETICAL: No

; FRAGMENT TYPE: Complete Sequence

; ORIGINAL SOURCE:

; ORGANISM: Homo sapien

; PUBLICATION INFORMATION:

; AUTHORS: Anderson, Stephen K.

; AUTHORS: Gibbs, Carol P.

; AUTHORS: Tanaka, Akio

; AUTHORS: Kung, Hsing-Jien

; AUTHORS: Fujita, Donald J.

; TITLE: Human Cellular src Gene:

; TITLE: Nucleotide Sequence and Derived Amino

; TITLE: Acid Sequence of the Region Coding for

; TITLE: the Carboxy-Terminal Two-Thirds of

; TITLE: pp60c-src

; JOURNAL: Molecular and Cellular Biology

; VOLUME: 5

; ISSUE: 5

; PAGES: 1122-1129

; DATE: May, 1985

; PUBLICATION INFORMATION:

; AUTHORS: Tanaka, Akio

; AUTHORS: Gibbs, Carol P.

? AUTHORS: Arthur, Richard R.
? AUTHORS: Anderson, Stephen K.
? AUTHORS: Kung, Hsing-Chen
? AUTHORS: Fujita, Donald J.
? TITLE: DNA Sequence Encoding the
? TITLE: Amino-Terminal Region of the Human c-src
? TITLE: Protein: Implications of Sequence
? TITLE: Divergence among src-Type Kinase
? TITLE: Oncogenes
? JOURNAL: Molecular and Cellular Biology
? VOLUME: 7
? ISSUE: 5
? PAGES: 1978-1983
? DATE: May, 1987
? US-07-820-011A-4

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Thu Jun 6 11:19:50 2002

us-09-444-7.

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2002, 08:26:28 ; Search time 213.19 Seconds
(without alignments)
12974.104 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

5. ched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1269	78.8	1699	AA587965	DNA encoding novel
3	1218.2	75.6	1759	AA228700	Wild-type chicken
4	1218.2	75.6	1759	AAH28357	Nucleotide sequenc
5	1216.6	75.5	1602	AAQ46687	Chicken pp60 c-src
6	1058	65.7	1090	AA587964	DNA encoding novel
7	908	56.4	3299	AAH18556	Human cDNA sequence
8	811.2	50.4	2433	AA594859	Human DNA sequence
9	710.2	44.1	4517	AAH30200	Human yes1 encodin

10	710.2	44.1	4517	AAH28359	Nucleotide sequenc
11	710.2	44.1	4517	AA574489	DNA encoding novel
12	574.8	35.7	2032	AA246491	PKA substrate, Src
13	539.8	33.5	1804	AA71262	Human c-yes-2 gene
14	539.8	33.5	1804	AAV20462	Human c-yes oncoge
15	539.8	33.5	1804	AAZ60825	Nucleotide sequenc
16	483.2	30.0	1254	AAQ33983	Lck gene fused wit
17	465.8	28.9	1491	AAZ08792	Human src-family k
18	465.8	28.9	1491	AAZ08746	Xenopus laevis src
19	464.2	28.8	1491	AA514754	Xenopus laevis src
20	464.2	28.8	1491	AA514755	Xenopus laevis src
21	425.2	26.4	2293	ABL01921	Drosophila melanog
22	425.2	26.4	2422	ABL019793	Drosophila melanog
23	407.6	25.3	2429	ABL02281	Drosophila melanog
24	386.6	24.0	2320	AA586451	DNA encoding novel
25	346.2	21.5	1574	AA286794	Human protein kina
26	346.2	21.5	1574	AAAD11845	Human protein kina
27	344.2	21.4	2507	AAQ81189	Breast tumour kina
28	344.2	21.4	3527	AA56986	DNA encoding novel
29	344.2	21.4	7487	AA52457	DNA encoding novel
30	341.6	21.2	780	AAZ08795	Human src-family k
31	341.6	21.2	780	AA514749	Src-family kinase
32	333.6	20.7	762	AAH06713	Human cDNA clone (
33	315	19.6	2152	AA592455	DNA encoding novel
34	314.4	19.5	3127	AA580650	DNA encoding novel
35	314	19.5	3026	AA592456	DNA encoding novel
36	296.2	18.4	1548	AAV81743	Human SAD encoding
37	284	17.6	7607	AAQ49754	PKC gene LpRK-2.
38	284	17.6	7607	AAH03097	Protein tyrosine-k
39	260	16.1	4515	ABL07083	Drosophila melanog
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41	256	15.9	5520	AA761865	c-abl gene. Homo
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45	239.8	14.9	1056	AAH18064	Lung cancer associ

ALIGNMENTS

RESULT 1

AAQ46688 standard; cDNA to mRNA; 1611 BP.

AAQ46688;

23-DEC-1993 (first entry)

Human pp60 c-src gene.

Endothelial, tyrosine kinase protein; pp60 c-src; ss.

Homo sapiens.

WO9314193-A.

22-JUL-1993.

05-JAN-1993; 93WO-US000445.

06-JAN-1992; 92US-0820011.

(UYVA) UNIV YALE.

Bell L, Luthringer DJ, Madri JA, Warren SL;

WPI; 1993-243209/30.

P-PSDB; AAR39705.

Genetically engineered endothelial cells - which exhibit enhanced
cell migration, urokinase-type plasminogen activator activity,
and reduced mononuclear cell adhesion and fibronectin produ

AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

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Ratio: 5.287 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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J9-444-711-1 x US-07-820-011A-4

Align seg 1/1 to: US-07-820-011A-4 from: 1 to: 536

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51 SerAlaAlaPheAlaProAlaAlaGlnProLysLeuPheGlyGlyPh 67
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PD	30-MAR-2001; 2001WO-US08631.
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PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
PA	(HWE-) HWESEQ INC.
PI	Drimanac RT, Liu C, Tang YT;
XX	
DR	WPI; 2001-639362/73.
P-PSDB:	ABG23778.
PT	New isolated polynucleotide and encoded polypeptides, useful in
XX	diagnostics, forensics, gene mapping, identification of mutations
XX	responsible for genetic disorders or other traits and to assess
XX	biodiversity -
PS	Claim 1; SEQ ID NO 23769; 103pp; English.
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
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: APPLICANT: Bell, Leonard
: APPLICANT: Madril, Joseph A.
: APPLICANT: Warren, Stephen L.
: APPLICANT: Luthinger, Daniel J.
: TITLE OF INVENTION: Genetically Engineered
: TITLE OF INVENTION: Endothelial Cells
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Maurice M. Klee
: STREET: 1951 Burr Street
:
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 760 Kb storage
: COMPUTER: DELL 486/50
: OPERATING SYSTEM: DOS 5.0
: SOFTWARE: Displaywrite 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00445
: FILING DATE: 19930105
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/820,011
: FILING DATE: 06-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: ALX-101PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 255 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 536 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: Linear
: MOLECULE TYPE: Protein
: HYPOTHEICAL: No
: FRAGMENT TYPE: Complete Sequence
: ORIGINAL SOURCE:
: ORGANISM: Homo sapien
: PUBLICATION INFORMATION:
: AUTHORS: Anderson, Stephen K.
: AUTHORS: Gibbs, Carol P.
: AUTHORS: Tanaka, Akio
: AUTHORS: Kung, Hsing-jien
: AUTHORS: Fujita, Donald J.
: TITLE: Human Cellular src Gene:
: TITLE: Nucleotide Sequence and Derived Amino
: TITLE: Acid Sequence of the Region Coding for
: TITLE: the Carboxy-Terminal Two-Thirds of
: JOURNAL: pp60c-src
: VOLUME: 5
: ISSUE: 5
: PAGES: 1122-1129
: DATE: May, 1985
: PUBLICATION INFORMATION:
: AUTHORS: Tanaka, Akio
: AUTHORS: Gibbs, Carol P.
: AUTHORS: Arthur, Richard R.
: AUTHORS: Anderson, Stephen K.
: AUTHORS: Kung, Hsing-jien
: AUTHORS: Fujita, Donald J.
: TITLE: DNA Sequence Encoding the
: TITLE: Amino-Terminal Region of the Human c-src
: TITLE: Protein: Implications of Sequence
: TITLE: Divergence among src-Type Kinase
: JOURNAL: Molecular and Cellular Biology
: VOLUME: 7
: ISSUE: 5
: PAGES: 1978-1983
: DATE: May, 1987
: PCT-US93-00445-4
:
: alignment_scores:
: Quality: 2834.00 Length: 536
: Ratio: 5.287 Gaps: 0
: Percent Similarity: 100.000 Percent Identity: 100.000

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Db 472 tccgagcggctgctgctcaacccccgaacccccggggaaccttctgtccgggagagc 531
 Qy 541 gagaccacgaagaagtgctactgctcctcagtgctgacttcgacaagcgaagggctc 600
 Db 532 gagacgaacaagaagtgctactgctcctcagtgctgacttcgacaagcgaagggctc 591
 Qy 601 aacgtgaagcactacaagatccgcaagctggaacggcgagcttctacatcacctccgc 660
 Db 592 aatgtgaagcactacaagatccgcaagctggaacggcgagcttctacatcacctccgc 651
 Qy 661 acccaggttaaacagcctggaacggcgagcttctacatcacctccgc 720
 Db 652 acccaggttgaagcctggaacggcgagcttctacatcacctccgc 711
 Qy 721 tcccaacggcctcaacggcgagcttctacatcacctccgc 780
 Db 712 tcccaacggcctcaacggcgagcttctacatcacctccgc 771
 Qy 781 gatgcttggaagatccctcggagtgctgctgagtgagtgcaagctgagcggagctc 840
 Db 772 gagcgctgggaatcccccggagtgctgctgagtgagtgcaagctgagcggagctc 831
 Qy 841 ttggcgagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 900
 Db 832 ttggcgagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 891
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 Db 892 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 951
 Qy 961 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1020
 Db 952 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1011
 Qy 1021 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1080
 Db 1012 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1071
 Qy 1081 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1140
 Db 1072 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1131
 Qy 1141 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1200
 Db 1132 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1191
 Qy 1201 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1260
 Db 1192 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1251
 Qy 1261 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1320
 Db 1252 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1311
 Qy 1321 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1380
 Db 1312 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1371
 Qy 1381 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1440
 Db 1372 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1431
 Qy 1441 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1500
 Db 1432 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1491
 Qy 1501 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1560
 Db 1492 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1551
 Qy 1561 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1611
 Db 1552 aagcctggaagtgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1602

RESULT 6
 AAS87964
 ID AAS87964 standard; CDNA; 1090 BP.
 XX
 AC AAS87964;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #23768.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG23777.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID No 23768; 103bp; English.
 PS
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1090 BP; 219 A; 331 C; 344 G; 196 T; 0 other;
 XX
 Query Match 65.7%; Score 1058; DB 23; Length 1090;
 Best Local Similarity 100.0%; Pred. No. 1.9e-190;
 Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 554 gtgctactgagctcctcagtgctgacttgacaaagcgaagggcctcaacgtgaagcact 613
 Db 1 gtgctactgagctcctcagtgctgacttgacaaagcgaagggcctcaacgtgaagcact 60

PCT-US93-06251-77

Query Match 42.8%; Score 689.4; DB 5; Length 2647;
Best Local Similarity 69.6%; Pred. No. 3.2e-131;
Matches 952; Conservative 0; Mismatches 406; Indels 9; Gaps 1;

QY 253 ggaatgacacacattgttgccctctatgactatgactagtagagagagagacacgtctcc 312
DB 826 GGAAGTGAACCTTTGTGGCCCTTTATGACTATGAAAGCAGCAGCAAGATGACCTGACT 885
QY 313 ttcaagaagagcagagcgtcccaagatgtcaacaacagagagagagcgtgtgctgagc 372
DB 886 TTTTCAAGAGAGAAATTTCAATATTTGAACAGCTCGAAGAGAGATTGTGGGAAGCC 945
QY 373 cactgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 432
DB 946 CGCTCCTTGACACTGGAGAGACAGGTTACCTCCAGCAATTAATGTGCTCAGTTGAC 1005
QY 433 tccatccagcgtgag 492
DB 1006 TCTATCCAGGAGAGAGATGATGCTTTGAAATTTGGCCGCAAAAGATGCTGACGACAG 1065
QY 493 ctgctcaatgag 552
DB 1066 CTATGTCCTTTGGAAACCCAGAGTACCTTTCTTATCCGAGAGAGTAAACACACAAA 1125
QY 553 ggtgcctactgctcctcagtgctgactcgaacagcagcagcagcagcagcagcagc 612
DB 1126 GGTGCTTATCCTTTGATCCGATGATGATGATGATGATGATGATGATGATGATGAT 1185
QY 613 tacaagatccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 672
DB 1186 TATATAATTCGAAACCTTGACAAATGATGATGATGATGATGATGATGATGATGAT 1245
QY 673 agcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 732
DB 1246 ACATTTGACGAGCTTTGATCAACATTAATCAAGAGAGAGAGAGAGAGAGAGAGAG 1305
QY 733 accacagcgtgccccagcagcagcagcagcagcagcagcagcagcagcagcagc 783
DB 1306 GTAGTCCCTGTCACAAAGAGAGATGCCAAGGCTTACGATCTGTCTCAAAACCAAGAT 1365
QY 784 gctcgtgagagatccctcagagagagcgtgctgagcagcagcagcagcagcagcagc 843
DB 1366 GTCTGGGAAATCCCTCGAATCCCTCGAATGATCAAGAGAGAGAGAGAGAGAGAT 1425
QY 844 ggcagagtggtgag 903
DB 1426 GGGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485
QY 904 cctgagcagatgctcagagagcctcctcagagagagagagagagagagagagagag 963
DB 1486 CCAAGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
QY 964 catgagagagcgtgag 1023
DB 1546 CACGACAGAGCTGTCACAGCTTATGACAGTGTGTGTGAGAGAGAGAGAGAGAGAG 1605
QY 1024 gagtagatgagcag 1083
DB 1606 GAGTATATGAAACAAAGAGAGATTTACTGATTTCTTAAAGATGAGAGAGAGAGAG 1665
QY 1084 cagctgctcagcgtgag 1143
DB 1666 AATATACCAATCTTGTGACATGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1725
QY 1144 cagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1203
DB 1726 CGCATGATATATATCATAGAGATCTGAGATCAGCAAAATTCATGAGAGAGAGAG 1785
QY 1204 gttgcaaaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1263

DB 1786 ATATGCAAGATTTGCTGATCTGATGATGATGATGATGATGATGATGATGATGAT 1845
QY 1264 cggcaaggtgccaattccccaatcagtgagcagcagcagcagcagcagcagcagcagc 1323
DB 1846 AGCAAGAGTGAAGATTTCCCATCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1905
QY 1324 ttaccatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1383
DB 1906 TTTCAATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1965
QY 1384 ggaaggtgccccctcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1443
DB 1966 GGAAGAGTGCATACCCAGCAGCATGAACAAACGGAGAGAGAGAGAGAGAGAGAGAG 2025
QY 1444 taccagatgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1503
DB 2026 TACAGAGTCCCTGAG 2085
QY 1504 tggcgaagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1563
DB 2086 TGAAAAAG 2145
QY 1564 tactcagctccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1610
DB 2146 TACTTTACCGGACAG 2192

RESULT 7
US-08-306-691B-40
; Sequence 40, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavourga & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEFAX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1804 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-306-691B-40.

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QY 808 ctgcggctgagagtcgaagctggccagggctgctttgycgaagtgatgagggagcttg 867
Db 454 ctgcggctgagagtcgaagctggccagggctgctttgycgaagtgatgagggagcttg 513
QY 866 aacggagacacacagagtgagcaccacaaacctgaagctggcagatgtctccagagcc 927
Db 514 aacggagacacacagagtgagcaccacaaacctgaagctggcagatgtctccagagcc 573
QY 928 ttccctcgaagagccagagtcacatgaagaagctgagcatgagaagctggcgagttat 987
Db 574 ttccctcgaagagccagagtcacatgaagaagctgagcatgagaagctggcgagttat 633
QY 988 gctgtggttcagagagagccacattacatgctacagagatcacatgacagggagattg 1047
Db 634 gctgtggttcagagagagccacattacatgctacagagatcacatgacagggagattg 693
QY 1048 ctggaactttcgaaggggagagacaggaagctacgtcgctgctcgaagctgtgagatg 1107
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Db 874 ctggtcgtcgtcattgaagaacaaatgatacaacgagcaggaagtgccaaatcccatc 933
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QY 1528 cccacactcgaatcctggaagccttccctggagagacttcaagcgcacagcccccag 1587
Db 1174 cccacactcgaatcctggaagccttccctggagagacttcaagcgcacagcccccag 1233
QY 1588 taccagcccgaggagaaactctag 1611
Db 1234 taccagcccgaggagaaactctag 1257

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RESULT 8
AAS94859
ID AAS94859 standard; DNA; 2433 BP.

AC AAS94859;
DT 14-FEB-2002 (first entry)
DE Human DNA sequence #114 expressed during foam cell differentiation.
KW Human, foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
OS Homo sapiens.
XX

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PN WO200177389-A2.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US11128.
XX
XX 05-APR-2000; 2000US-195106P.
XX
XX (INCYTE GENOMICS INC.
PA
PI Shiffman D, Somogyi R, Lawn R, Sellhammer JU, Porter GJ, Mikita T;
PI Tai J;
PI
XX
XX WPI; 2002-010925/01.
XX
XX
XX The present invention relates to the isolation of human polynucleotide
XX sequences that are differentially expressed during foam cell
XX differentiation. The polynucleotide sequences of the invention or a
XX composition comprising these polynucleotides are useful as a high
XX throughput method for detecting altered expression of one or more
XX polynucleotides in a sample. The polynucleotides can be used in the
XX diagnosis of disorders associated with foam cell development such as
XX atherosclerosis, cerebral stroke, and cardiovascular disorders such as
XX coronary artery disease. The polynucleotide sequences can also be used
XX as PCR primers and probes. The polynucleotides of the invention are also
XX useful in gene therapy. AAS94746-AAS95021 represent the human
XX polynucleotide sequences of the invention which are differentially
XX expressed during foam cell differentiation.
XX
XX Sequence 2433 BP; 547 A; 676 C; 687 G; 523 T; 0 other;

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Query Match 50.4%; Score 811.2; DB 24; Length 2433;
Best Local Similarity 73.9%; Pred. No. 6.2e-144;
Matches 1029; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

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QY 220 acctcccgaagggggggccgctgctgctgagtgatgacaccttggccctcat 279
Db 267 acctcgtgtagtgccttgcctctgcagggatgtgggtgacccgttattgacctgcat 326
QY 280 gactatagctctgagagggagacacactgtccttcaagaagggcagcgctccagatt 339
Db 327 gactatgaggtcgaactgtgagatgacactccttcaagaagggcagaaattccaacac 386
QY 340 gtacaacacagagggagacatgtgtgctgcccactcgtcgaacagacagacagacagc 399
Db 387 ctgaacataactgaagtgactgtgtgagagctcgtcctccagctccggaaactgtgc 446
QY 400 tacatcccacgaacatcgtgtgcccctccgactccatccagagctgagagtgatttt 459
Db 447 tgcattcccacgaactcagtggtccctgtgactccaatccaagctgaagatgtgacttt 506
QY 460 ggcagaatcacccagagcggtcagagcgtttactgtcattcgaatgagaagaaccgagag 519
Db 507 ggaagaacttggagaaagatgacagagagcagagctgttcaacaggaaccgccagggg 566
QY 520 accttcctgtgagaaatgagacacagaaagtgtcctactcgtcctcagtgctgac 579
Db 567 gcttctcattcgtggagaaagcagacacaaagtgtcctactcctcgtcctacccggac 626
QY 580 ttgcagaacgcaagggcctcaacgtgaagcactacaagaatccgaaagctgagacagcg 639
Db 627 tggatcagaccagagcgatcattgaagcattacaagaatccgaaactgagatggc 686
QY 640 ggcttctacacctcccgacaccagttacaagcctgtcagacagctggtggctactac 699
Db 687 ggtactaatcacacacacaggttcaactcgtgtcagagagcgtgtgacagactac 746

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Db 656 cagattccattcaaggcagaagaatggtatttgcacaatgaggagaaagatgctgaa 715
 Oy 488 ggttactgtcaatgacagaaacccgagagggaaccttcctcgtgcgagaaagtgaacca 547
 Db 716 gattacttttgatccatggaataacagagatcttcttagtaaaagagatgaacaa 775
 Oy 548 cgaagagtgccactgacctcagtgctgacttcgacaacgccaaggcctcacaagctga 607
 Db 776 ctaaaagtgctattcccttcttctatcgtgatggaatgaaagaggtgacaatgga 835
 Oy 608 agcactacaagatccgcaagctggaagcggcgtcttacaacctcccgaccagat 667
 Db 836 aacactacaaatlagaaactctggaactcgtggaatctatcatatcacacagagcacaat 895
 Oy 668 tcaaacgctgacagacgctggtggtgactactacacaacgctgactgctgaccac 727
 Db 896 ttgatactctgagaagaattggtgaaacactacacagaaatctgattgttttagccaca 955
 Oy 728 gacctacacacgctggtccacgctcgaagcgcgacactcagggcctggtccaaagatgct 787
 Db 956 agtgacacactggtgtccaaactggaaccccgacactcaaggtctcagcaaaagatgctt 1015
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 Db 1016 gggaaatccctcgaagaatcttgcgactagaggttaactagacagatgtttccgcg 1075
 Oy 848 agtggtgagtgggaacctggaacggtaccacagaggtggtccataaacctgaaagctg 907
 Db 1076 aagtggtgagtgaacatggaatggaacacagaaagtagcaatcaaacataaaccaag 1135
 Oy 908 gacgagtcttccaaagccttcctcgcagagagccaggtcatgaaagcctgagacatg 967
 Db 1136 gtacaatgtgcgaagaaccttccctcacaagaagctcagaataagaaataaagacatg 1195
 Oy 968 aagaactgtgacgtgtgatactggtgtgttcagaggagcccttaccgtgacagagat 1027
 Db 1196 ataactgttccactatatactgtgtgttctcgaagaaacaaattacatgtacatgcaaat 1255
 Oy 1028 acatgagcaaggggaggttgcgtgcgaacttctcaagggggagacaggaactacgtgcgc 1087
 Db 1256 ttatgtcaaaaggaagctatttagatttcccttaaggaagagatggaagattttagaagc 1315
 Oy 1088 tgcctcaagctggtgacatggtgctgcacagatgcgtcgaagcgtgcgtgagagcga 1147
 Db 1316 ttccaagctggtgtatgtgtgctgcacagatgctgatatgtatgcatatttgaagaa 1375
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 Oy 1208 gcaaaagtgcgcgaacttgggtgcgtgcgtcatatgaaacaaatgatacagggcgcg 1267
 Db 1436 gcaaaatagcagacttggtttagcaaggttaattgaagaacatgatacacaagcagac 1495
 Oy 1268 aaggtgccaattcccatcaagtgaagcgtccagaagcgtccctctatgagcgcttca 1327
 Db 1496 aaggtgcaaaatttccaatcaaatgacagcctcgaagcgtcactgtatgctgagttta 1555
 Oy 1328 ccatcaagctgagcgtgtgctcgtgcgatactgctgctgagctcacacaagaaggagc 1387
 Db 1556 caataaagatcgtatgtctggtcaatttgaatcttgcacaacagaacagtaacaaaggcc 1615
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 ID AAH28359 standard; cDNA; 4517 BP.
 XX
 AC AAH28359;
 XX
 DT 05-SEP-2001 (first entry)
 XX
 DE Nucleotide sequence of human tyrosine kinase protein Yes.
 XX
 KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
 KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
 KW diabetic retinopathy; inflammatory disease; infection; arthritis;
 KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
 KW diabetic retinopathy; psoriasis; neovascular glaucoma;
 KW capillary proliferation; osteoporosis; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 208..1839
 FT /*tag- a
 FT /*product= "Yes"
 XX
 PN WO200145751-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000MO-US35396.
 XX
 PR 22-DEC-1999; 9905-0470881.
 PR 29-MAR-2000; 2000US-0538248.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Cheresah DA, Elliceiri B, Paul R;
 PI
 DR WPI; 2001-417982/44.
 DR P-PDB; AAB84663.
 XX
 PT Modulating vascular permeability in tissues, including inflamed tissue,
 PT tissues associated with stroke, myocardial infarction, by contacting
 PT the tissue with tyrosine kinase protein Src, Yes or their modified
 PT forms
 XX
 PS Disclosure; Fig 12; 133pp; English.
 XX
 CC The specification describes a method for modulating vascular
 CC permeability in a tissue suffering from a disease condition. The method
 CC comprises contacting the tissue with a pharmaceutical composition
 CC comprising tyrosine kinase protein Src, Yes or their mixtures or
 CC nucleic acid expressing them. The method is useful for modulating
 CC vascular permeability in tissues, including inflamed tissue, tissues
 CC associated with stroke, myocardial infarction or other blockage of
 CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
 CC and similar tissues. Pathologies which may be treated include atherosclerosis,
 CC trauma to blood vessels, and other systemic pathological events such as
 CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
 CC infection by microbial agents and arthritis. Other diseases which can
 CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
 CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
 CC capillary proliferation in atherosclerotic plaques and osteoporosis and
 CC cancer associated disorders such as solid tumours, solid tumour
 CC metastases, angiofibromas and hemangiomas. The present sequence
 CC encodes human Yes, and is used in the method of the invention.
 CC
 XX

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821 TCAGCTGGGGCCAGGGCTGCTTGGCAGGTGTGATGGGAGACTGGAAC 870
281 allLysLeuGlnGlnLysCysPheGlyGluValTrpMetGlyThrTrpAsn 297
871 GGTACACCAAGGGTGGCTGATCAAAACCTGAGCCTGGACGATGTCTCC 920
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971 AGCTGTGCAAGTTGATGCTGTGTTTCAAGAGAGCCCATTTACATGCTC 1020
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XX      05-SEP-2001 (first entry)
DT
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XX      Amino acid sequence of human tyrosine kinase protein yes.
DE
XX
XX      Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW      myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW      diabetic retinopathy; inflammatory disease; infection; arthritis;
KW      adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW      diabetic retinopathy; psoriasis; neovascular glaucoma;
KW      capillary proliferation; osteoporosis; cancer.
XX
XX      Homo sapiens.
OS
XX
XX      MO200145751-A1.
PN
XX
XX      28-JUN-2001.
PD
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XX      22-DEC-2000; 2000MO-US35396.
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XX      22-DEC-1999; 99US-0470881.
PR
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PA
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XX      Chersesh DA, Ellicelrl B, Paul R;
PI
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XX      WPI: 2001-417982/44.
DR
XX      N-PSDB; AAH28359.
XX
XX      Modulating vascular permeability in tissues, including inflamed tissue,
PT      tissues associated with stroke, myocardial infarction, by contacting
PR      the tissue with tyrosine kinase protein Src, Yes or their modified
PS      forms
XX
XX      Disclosure; Fig 11; 133pp; English.
PS
XX
XX      The specification describes a method for modulating vascular
CC      permeability in a tissue suffering from a disease condition. The method
CC      comprises contacting the tissue with a pharmaceutical composition
CC      comprising tyrosine kinase protein Src, Yes or their mixtures or
CC      nucleic acid expressing them. The method is useful for modulating
CC      vascular permeability in tissues, including inflamed tissue, tissues
CC      associated with stroke, myocardial infarction or other blockage of
CC      normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC      and similar tissues. Pathologies which may be treated include include
CC      trauma to blood vessels, and other systemic pathological events such as
CC      atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC      infection by microbial agents and arthritis. Other diseases which can
CC      be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC      arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC      capillary proliferation in atherosclerotic plaques and osteoporosis and
CC      cancer associated disorders such as solid tumours, solid tumour
CC      metastases, angiofibromas and hemangiomas. The present sequence
CC      represents human Yes, and is used in the method of the invention.
XX
XX      SO      Sequence      543 AA:

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alignment_scores:

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Quality: 2123.50      Length: 546
Ratio: 4.480          Gaps: 4
Percent Similarity: 86.813      Percent Identity: 74.542

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alignment_block:

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US-09-444-711-1 x AAB84663
Align seg 1/1 to: AAB84663 from: 1 to: 543

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2002, 08:26:28 ; Search time 54.19 Seconds
(Without alignments)
7302.373 Million cell updates/sec.

Title: US-09-444-711-1

Perfect score: 1611

Sequence: 1 atgggtacacacagagacaa.....agcccgaggagacacctag 1611

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Se-ched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

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6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609.4	99.9	1611	1	US-07-820-011A-3 Sequence 3, Appl
2	1609.4	99.9	1611	5	PCT-US93-00445-3 Sequence 3, Appl
3	1216.6	75.5	1602	1	US-07-820-011A-1 Sequence 1, Appl
4	1216.6	75.5	1602	5	PCT-US93-00445-1 Sequence 1, Appl
5	710.2	44.1	4517	5	PCT-US93-06251-83 Sequence 83, Appl
6	689.4	42.8	2647	5	PCT-US93-06251-77 Sequence 77, Appl
7	539.8	33.5	1804	1	US-08-306-691B-40 Sequence 40, Appl
8	539.8	33.5	1804	5	PCT-US93-06251-82 Sequence 82, Appl
9	465.8	28.9	1491	2	US-09-006-675-1 Sequence 1, Appl
10	465.8	28.9	1491	4	US-09-228-603A-1 Sequence 1, Appl
11	346.2	21.5	1574	3	US-09-173-581-12 Sequence 12, Appl
12	346.2	21.5	1574	4	US-09-420-915-12 Sequence 12, Appl
13	341.6	21.2	780	2	US-09-006-675-7 Sequence 7, Appl
14	341.6	21.2	780	4	US-09-228-603A-7 Sequence 7, Appl
15	284	17.6	2770	4	US-08-426-509A-5 Sequence 5, Appl
16	284	17.6	2770	5	PCT-US95-05008-5 Sequence 5, Appl
17	284	17.6	7607	1	US-08-222-616-19 Sequence 19, Appl
18	284	17.6	7607	5	PCT-US95-04228-19 Sequence 19, Appl
19	252	15.6	271	1	US-08-306-691B-24 Sequence 24, Appl
20	252	15.6	271	5	PCT-US93-06251-66 Sequence 66, Appl
21	249.6	15.5	3623	1	US-08-306-691B-35 Sequence 35, Appl
22	217.6	13.5	728	4	US-09-328-111-821 Sequence 821, App
23	212.4	13.2	1398	2	US-08-604-989A-9 Sequence 9, Appl
24	212.4	13.2	1521	2	US-08-604-989A-10 Sequence 10, Appl
25	212.4	13.2	1942	2	US-08-604-989A-11 Sequence 11, Appl
26	212.4	13.2	2000	4	US-08-426-509A-11 Sequence 11, Appl
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28	210.8	13.1	255	1	US-08-306-691B-34	Sequence 34, Appl
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34	200	12.4	1987	2	US-08-876-882-1	Sequence 1, Appl
35	182	11.3	194	1	US-08-306-691B-30	Sequence 30, Appl
36	182	11.3	194	5	PCT-US93-06251-72	Sequence 72, Appl
37	181.2	11.2	2505	1	US-08-391-615-1	Sequence 1, Appl
38	170.4	10.6	2674	4	US-09-817-180-1	Sequence 1, Appl
39	165	10.2	3546	1	US-08-162-809-9	Sequence 9, Appl
40	165	10.2	3591	1	US-08-162-809-13	Sequence 13, Appl
41	162.6	10.1	2962	2	US-08-445-645A-10	Sequence 10, Appl
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45	161	10.0	4097	1	US-08-162-809-11	Sequence 11, Appl

RESULT 1
US-07-820-011A-3
Sequence 3, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: and Plasmidogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: 1B-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 20

DB 1561 GACTACTTCAGTCCACCGAGCCCACTACCAAGCCCGGAGAACCTCTAG 1611

RESULT 2

PCT-US93-00445-3
Sequence 3, Application PC/TUS9300445

GENERAL INFORMATION:

APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA

ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 20
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.

AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
PCT-US93-00445-3

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INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:
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 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-0593-06251-83

Query Match 44.1%; Score 710.2; DB 5; Length 4517;
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 728 gctcaccacagctgt 787
 Db 956 AGTTGCAACTGTGTGTCTCAACTGTAACCTGAGACTCAAGCTCAAGCAAAAGATGCTT 1015
 788 gggagatccctcggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 847
 Db 1016 GGGAAATCCCTGAGAAATTTTGGCACTAGAGGTTAAACTAGAGCAAGGATGTTGGCGC 1075
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 Db 1256 TTATGTCAAAAGGAAGCTTATTAAGATTTCTTAAGAGAGAGATGGAATATTGTAAGC 1315
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 Db 1316 TTCCACAGCTGTGTATATGCTGTGCTCAGATTCCTGATGATGATGATTAATTAAGAA 1375

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 Qy 1208 gcaagtgccagctgt 1267
 Db 1436 GCAAAATAGCAGACTTGT 1495
 Qy 1268 aagtgcccaatttcccatcaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1327
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RESULT 6
 PCT-US93-06251-77
 Sequence 77: Application PC/TUS9306251
 GENERAL INFORMATION:
 APPLICANT: Wickstrom, Eric and Rife, Jason P.
 TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
 TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: USA
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06251
 FILING DATE: 19930630
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DiGiullo, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 8586
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2647 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

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QY	984	gtatgc---tggtgttcagaagagagccattatcatctgcagagtaacttgagcaagg	1044
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<p>RESULT 10 US-09-228-603A-1 : Sequence 1, Application US/09228603A : Patent No. 6291651 : GENERAL INFORMATION: : APPLICANT: Hemmati-Brivanlou, Ali : APPLICANT: Weinstein, Daniel C. : TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF : NUMBER OF SEQUENCES: 12 : CORRESPONDENCE ADDRESS: : ADDRESSEE: Klauber & Jackson : STREET: 411 Hackensack Avenue, 4th Floor : CITY: Hackensack : STATE: New Jersey : COUNTRY: USA : ZIP: 07601 : COMPUTER READABLE FORM: : MEDIUM TYPE: Floppy disk : COMPUTER: IBM PC compatible : OPERATING SYSTEM: PC-DOS/MS-DOS : SOFTWARE: Patentin Release #1.0, Version #1.30 : CURRENT APPLICATION DATA: : APPLICATION NUMBER: US/09/228,603A</p>			

FILING DATE: 12-JAN-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-217 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1491 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1491

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seq_documentation_block:

Sequence 13, Application US/08426509A

ent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Gshlezky, Mikhail

APPLICANT: Sures, Irman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 536 amino acids

TYPE: amino acid

STRANDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: No. 6326469e

US-08-426-509A-13

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Ratio: 5.287 Gaps: 0

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151 AGCGCGCGCTTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 200
51 SerAlaAlaPheAlaProAlaAlaAlaGluProLysLeuPheGlyGly 67
201 CAACCTCTCGGACACCGGTACCTCCCGCGAGAGCGCGCGCGCGCG 250
67 eaSnSerSerAspThrValThrSerProGlnArgAlaGlyProLeuAla 84
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84 LysIValThrThrPheValAlaLeuTyrAspTyrGluSerArgTrpGlu 100
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17 rLeuGlnProAlaGlnAsnValHisGlnAlaGlyGlyAlaPhePro 34
101 CCTCGCAGACCCCAAGCAAGCCAGCTCGCGCCAGCCAGCCAGCGCGCC 150
34 laSerGlnThrProSerLysProAlaSerAlaAspGlnHisArgGlyPro 50
151 AGCGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 200
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84 LylGlyValThrThrPheValAlaLeuThrAspTryGlnSerArgThrGln 100
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201 AsnValLysHisIleTryLysIleArgLysLeuAspSerGlyGlyPheTry 217
651 CACTTCCCGCAGCCAGTTCAAGCAAGCTGAGAGCGAGTGTGGCTACT 700
217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaIleTryLys 234
701 CCMAACAGCCGATGGCTGTGCGACCGCGCTCAGACCGGTGCGCCAG 750
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751 TCCAGACCCAGACTAGGCGCTGGCGCAAGAGTGCCTGGAGATCCCTG 800
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267 gGlnSerLeuArgLeuGlnValAlaLysLeuGlnGlnLysCysPheGlyGln 284
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seq_documentation_block:
; Sequence 13, Application PC/TUS9505008
; GENERAL INFORMATION:
; APPLICANT: Sugen, Inc.
; APPLICANT: 515 Galveston Drive
; APPLICANT: Redwood City, California 94063-4720
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ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-2

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Ratio: 5.107          Gaps: 1
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Align seg 1/1 to: PCT-US93-00445-2 from: 1 to: 533

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921 AGAGGCTCTCTGACAGAGGCCAGGTCATGAAGAAGCTGAGGATGAGA 970
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314 GGLuAlaPheLeuGlnGlnAlaGlnIleMetCysLysLeuArgHisAspL 331
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971 ACCTGGTCAGATTGTATGCTGTGGTTTCAGAGAGGCCATTTCATCAGTC 1020
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331 yLeuValPProLeuTyAlaValValSerGlnLupProIleTyAlaVal 347
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1021 ACGAGATACATGACAGAGGAGCTTTCGAGACTTTCCTCAGAGGGAGAC 1070
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348 ThrGluPheMetSerLysGlnSerLeuLeuAspPheLeuLysGlnLys 364
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364 polyLysTyLeuLysLeuProGlnLeuValAlaPheAlaAlaGlnLea 381
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381 laAspGlyMetAlaTyrlleGluArgMetCAsnTyrlleHisArgAspLeu 397
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398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLysIleAlaAs 414
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1221 CTTTGGGCTGCTGGCTCATGACAACAATGACTACAGCGCGCGCAAG 1270
|||||
414 PheGlyLeuAlaArgLeuIleGluAspAsnGlnTyrlleAlaArgGln 431
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1271 GTGCCAAATTCCTCCATCAGTGGAGCGCTCCAGAGCTGCTCTATGCG 1320
|||||
431 yAlaIlePheProIleTySTPrThAlaProGlnAlaAlaLeuTyrlle 447
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1321 CGCTTCACCATCAAGTCGAGCTGTGCTGCTGGAGATCCTGCTGACTGA 1370
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448 ArgPheThrIleLysSerAspValTrpSerPheGlyIleLeuGlnThrG 464
|||||
1371 GCTCAACCAAAAGGAGCGGGTGCCTACCTGGAGATGGTGAACCGGAGG 1420
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464 uLeuValThrLysGlyArgValProTyProGlyMetValAlaArgGln 481
|||||
1421 TGCTGACACAGGTGAGCGGGCTACCGGATGCTGCTGCGCGGAGTGT 1470
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481 aLeuGlnGlnIleValGlnArgGlyTyrlleArgMetProCysProGlnG 497
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1471 CCCGAGTCCCTGCAGACCTCATGTCCAGTGTGCGGAGAGAGAGCTGA 1520
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seq_documentation_block:
: Sequence 14. Application PC/TUS9505008
: GENERAL INFORMATION:
: APPLICANT: Sugen, Inc.
: APPLICANT: 515 Galveston Drive
: APPLICANT: Redwood City, California 94063-4720
: APPLICANT: United States of America
: APPLICANT: Missionschaften E.V.
: APPLICANT: Hofgarten Str. 2
: APPLICANT: Munchen 80539
: APPLICANT: Germany
: TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21

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: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Penile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05008
: FILING DATE: 24-APR-1995
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/232,545
: FILING DATE: 22-APR-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzel, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-074
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212)669-9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 543 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: PCr-US95-05008-14

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Percent Similarity: 86.813 Percent Identity: 74.542

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1 MetIlyCysIleLysSerLysGluAsnLysSerProAlaIleLysTyAlr 17
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48 CAGCCTGAGCGCCCGGAGAGCTGCAGCGCGCGCGG.....GGCG 91
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17 gProGlnsInThrProGlnProValSerThrSerValSerHisTyrlle 34
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34 laGluProThrThrValSerProCysProSerSerSerAla..... 47
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142 CGCGGGCCCGAGCGGCTTGCCTGCGCGCGCGCGAGCC..... 183
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48 LysGlyThrAlaValAlaAsnPheSerSerLeuSerMetThrProPheGly 64
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184 .....AAGCTGTGCGAGGCTTCAACTCCGCGAGCAACCTGCA 220
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64 ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerVal 81
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221 CCTCCCGCAGAGAGCGCGCGCTGCGCGGTGAGTACCACTTTGTG 270
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81 alProSerSerTyrlleProAlaGlyLeuThrGlyGlyValThrIlePheVal 97
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271 GCCCTATGACTATGACTTAGACGAGAGACGACTGCTCTTCAAGA 320

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1022 CGGAGTACATGAGCAGGAGGAGTTGCTGACCTTCTCAAGGGGAGACA 1071
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341 hrluphemetserInglyserleuaspheleuaspdglyasp 357
1072 GGCAGTACCTGCGGCGCTGAGCTGAGTGGTGGTCTGCTGAGTGGC 1121
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358 GLYhrgrtyrleuysleuProGlnleuValaspmetalaaglnlleal 374
1122 CTCAGGCGATGCGCTGAGCGGAGGATGAACTAGCTCACCGGAGACTTC 1171
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374 aalaglymetaleatyrillegluarqmetasnryillehsrgraspleua 391
1172 GTGCAGCCAAATCTCTGCTGGGAGAGAACTGTGTGCAAGTGGCCGAC 1221
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391 rglalaalaasnilleuValaglyaspasnleuValcyslysllealasp 407
1222 TTGGGGTGGCTGGCTCATTTGAAGACAATGATGACAGCGCGGCGCAAG 1271
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408 PheglyleuAlarglyleuIlegluaspsnslutyrThrAlaarglnGl 424
1272 TGGCAATTCCTCATCAAGTGGAGGCGCTCCAGAGCGCTCCCTCATGGCC 1321
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424 yAlaLysPheProIleLysTrpThrAlaProGlnAlaLeuPheglyL 441
1322 GCTTCACCATCAAGTGGAGTGGTGGTCTTCGGGATCGTGGTGGAG 1371
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1372 CTCACGACAAAGGAGCGGTGCCCTTACCTGGATGGTGAACCGCGAGT 1421
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1422 GCTGAGACAGAGTGGAGCGGGGCTACCGGATGCCGCCCGCGGAGTGC 1471
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474 lleuglnGlnValgluarqglytyrArqmetGlnCysProglyglyCysP 491
1472 CCGAGTCCCTGACAGACCTCATGTGCGAGTGGTGGGAGGAGCGCTGAG 1521
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1522 GAGCGGCGCCACTTCGAGTACCTGACGCGCTTCCTGGAGGAGTACTTAC 1571
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-594-447-1

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seq_documentation_block:
: Sequence 1, Application US/08594447
: Patent No. 5776716
: GENERAL INFORMATION:
: APPLICANT: Ron, Dorit
: APPLICANT: Napolitano, Eugene W.
: APPLICANT: Voronova, Anna F.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
: TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USBS
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/594,447
: FILING DATE: 31-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22550-20025.24
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 822-0168
: TELEX: 90-4030 MRSNFOERSM
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-594-447-1

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alignment_scores:
Quality: 1944.00 Length: 550
Ratio: 4.208 Gaps: 7
Percent Similarity: 84.000 Percent Identity: 68.545

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alignment_block:
US-09-444-711-1 x US-08-594-447-1

Align seg 1/1 to: US-08-594-447-1 from: 1 to: 532

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|||||
15 rGlnGlnArgaspGlySerleuasnGlnsererglytyrArqtyrGlyT 32
101 COTGCAACACCCGCAAGCCAGCCAGCCCTCG..... 129
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32 hrAspProThrProGlnInitrtyrProserPheglyValThrserlePro 48
130 .....GCGAGCGCCACCGCGCGCGCGCGCGCGCTT 161
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49 AsnTyraAsnAsnPheHIsAlaIleagllyglnglyleuthr..... 62
162 CGCCCGCGCGCGCGCGCGAGCCCAAGCTGTTCGAGGCTTCAACTCTCG 211
|||||
63 .....ValPheglylyValaIsnSerSers 71
212 AC...ACCGTACCTCCCGGAGGCGCGCGCGCGCTGCGCGGTGAGAG 258
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71 ernHsthrglyThrleuArqThrArqglyGlyThr.....GlyVal 84
259 AACACCTTTGTGGCCCTCTATGACTATGAGTCTAGACGAGAGACCT 308
|||||
85 ThrleuPheValAlaLeuTyraSptyr..AlaArgThrGlnaspSple 100
309 GTCTTCAAGAAAGCGAGCGGCTCCAGATTGTCAACAACAGCGAGGAG 358
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100 userPheHIsLysgllyGlnLysPheglIleleuasnserSerglnGlyA 117
359 ACTGTGCTGGCCGCTGCTGCTGACAGACAGAGACAGGCTTACATCCCG 408
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117 sTrpTrpGlnAlaArgSerleuThrThrGlyGlnThrGlytyrIlePro 133
409 AGCACTAGTGGCGCGCTCGACTCATTCAGGCTGAGAGAGTGTATT 458
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alignment_block:

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Align seg 1/1 to: US-08-665-647-1 from: 1 to: 532

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101 COTGCGACAGCCCGCAGACGCGCTCG..... 129
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63 .....ValPheGlyGlyValAsnSerSerS 71
212 AC...ACCGTCACCTCCCGCAGAGCGCGCGCGCGCGCGCGCTGAGT 258
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71 GlnHisThrGlyThrLeuArgThrArgGlyGlyThr.....GlyVal 84
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709 GCGCAGTGGCTGTGGCAGCGCTCACACGCGTGTGCCCGACGCGCAAGC 758
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759 GCAGACTACAGGCGCTGCGCAAGAGTCCCTGGAGATCCCTCGGAGACTCG 808
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249 cGlnThrSerGlyLeuAlaLysAspAlaTrpGlnValAlaIrgArgSerL 266

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809 TGGGCTGAGAGTCAAGCTGGGCGAGGCTGCTTGGCGAGGTGGATG 858
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859 GGGACCTGGAACGGTACCACAGGCTGGCCATCAAAACCTGAAGCTGG 908
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959 TGAAGCATGAGAACGTGTCAGATTGATGCTGTGTTTCAGAGAGCC 1008
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1009 ATTTACATCTCACAGAGTACATGAGCAAGGAGATTGCTGACCTTCT 1058
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seq_documentation_block:

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; Sequence 11, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Ilman G.

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1200 CCTGTGTGCAAGAGTGGCCGACTTGGGCTGGCTGGCTCATTTGAAGACA 1249
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418 snGluTyrThrAlaArgGlnGlnGlnAlaLysPheProIleLysThrAla 434
1300 CCAGAGGTGCTCTATGCGCGCTTCAACATCAAGTGAAGTGTGTC 1349
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1350 CTTCGGGATCTGCTGACTGACTGACCTACCAACAAAGGAGCGGTGCTAC 1399
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1400 CTGGGATGTGACCGGAGGTGCTGACACAGTGAAGCGGGGCTACCGG 1449
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1550 CCTCCCTGAGGAGACTACTTCACGTCACCGACCGGACCATACCGCCGG 1599
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535 GluAsnLeu 537

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seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.PCT-US95-05008-11

seq_documentation block:

Sequence 11, Application PC/TUS9505008

GENERAL INFORMATION:

APPLICANT: Sugen, Inc.

APPLICANT: 515 Galveston Drive

APPLICANT: Redwood City, California 94063-4720

APPLICANT: United States of America

APPLICANT: Wissenschaften E.V.

APPLICANT: Hofgarten Str. 2

APPLICANT: München 80539

APPLICANT: Germany

TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05008

FILING DATE: 24-APR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-11

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alignment_scores:

Quality	1932.50	Length	553
Ratio	4.201 <td>Gaps</td> <td>6</td>	Gaps	6
Percent Similarity	83.183	Percent Identity	67.812

alignment_block:

US-09-444-711-1 x PCT-US95-05008-11 ..

Align seg 1/1 to: PCT-US95-05008-11 from: 1 to: 537

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1 ATGGGTAGACACAGAGCAAGCCCAAGATGCCAGCGGCGCCGAC 50
      |||
1 MetGlyCysValGlnCysLysAspLysGluAlaThr....LysLeuTh 15
51 CCGGAGCCCGCGGAGAGCAGCGCGCGCGCGCGCGCTTCCCGC 100
      |||
15 rGluGluArgAspGlySerLeuAsnGlnSerSerGlyTyrArgTyrGly 32
101 CCTCGCAGACCCCGCAGACCGACCTCG..... 129
      |||
32 hrAspProThrProGlnHisTyrProSerPheGlyValThrSerIlePro 48
130 .....GCCAGGCGCACCGCGCGCCGCGCGCTT 161
      |||
49 AsnTyrAsnAsnPheHisAlaIleGlyGlnGlyLeuThr..... 62
162 CGCCCGCGGCGCGCGCGCAGCGCTGTCGAGCTTCACTTCCTCGG 211
      |||
63 .....ValPheGlyGlyValAsnSerSerS 71
212 AC...ACCGTCACCTCCCGCAGAGCGCGCGCGCGGTGGAGTG 258
      |||
71 erHisThrGlyThrLeuArgThrArgGlyGlyThr.....GlyVal 84
85 ThrLeuPheValAlaLeuTyrAspTyrGluAlaArgThrGluAspLe 101
309 GTCCTTCAAGAAAGCGGAGCGGCTCCAGATGTCACACACGAGGAGG 358
      |||
101 userPheHisLysGlyGluLysPheGlnIleLeuAsnSerSerGluLys 118
359 ACTGTGTGCTGCGCCACTGCTGACAGAGAGAGAGAGAGAGCTACATCC 408
      |||
118 sPThrProIleValAlaArgSerLeuThrThrGlyLysThrGlyTyrIlePro 134
409 ACCAATACGTGCGCGCTCCGACTCATCAGAGTGAAGAGTGAATTT 458
      |||
135 SerAsnTyrValAlaProValAspSerIleGlnAlaGluLysThrPyr 151
459 TGGCAAGATCACCAGAGCGGAGTCAAGCGGTTACTGCTCATGACAGAG 508
      |||

```

Percent Similarity: 83.962 Percent Identity: 67.170

alignment_block:

US-09-444-711-1 x US-08-426-509A-15

Align seg 1/1 to: US-08-426-509A-15 from: 1 to: 529

```

13 AAGAGCAAGCCCAAGATGCCAGCCAGCGGCGCCGAGCCTGAGACCCGC 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8 LysLeuGluProValAlaThrAlaLysGluAlaPheGluGluLys 24
63 CGAAGACGTGCACGCGCTGCGGGGGGCGCTTCCCGCCTCCGAGACC 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24 PheAspSerTyrGlyAlaAlaAspHisTyrGlyPro...AspProThrL 40
113 CCGAGCAAGCAGCCTGCGCGGCGAGCGGCGCGCCCGAGCGGCGCTTC 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 ValAlaArgProAlaSerSerPheAlaHisIleProAsnTyrSerAspPhe 56
163 GCCCGCGCGCGCGCGCCGAGCCCAAGCTGTTGCGAGGCTTCAACTCC 212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 SerSerGluAlaIleAsnPro.....GlyPheLeuAspSerG 69
213 CACCGTCACCTCCCGCAGAGGGCGGGCGCGCTGGCCGCTGAGTACCA 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
69 yThrIle.....ArgGlyValSerGlyIleGlyValThrL 81
263 CCTTTGTGCGCCTCTATGACTATGACTAGTCTAGACGAGACAGACTTC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 eupHeIleAlaLeuTyrAspTyrGluAlaArgTyrGluAspPheLeuThr 97
313 TTCACAAAGAGCGAGCGGCTCCAGATTGTCAACACACAGCGAGGAGACTG 362
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
98 PheThrLysGlyGluLysPheHisIleLeuAsnHisnThrGluGlyAspTr 114
363 GTGGCTGGCCCACTCGCTCAGACAGACAGACAGAGCTTACATCCCGCA 412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
114 pTrpGluAlaArgSerLeuSerSerGlyLysThrGlyCysIleProSerA 131
413 ACTACGTGGCGCCCTCCGACTCCATCCAGCGCTGAGAGTGATATTGGC 462
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
131 snTyrValAlaProValAspSerIleGlnAlaGluGluTyrPheGly 147
463 AAGATACACAGAGGAGTACAGCGGTTACTGCTCAATGCAGAGAACCC 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
148 LysIleGlyArgLysAspAlaGluAlaGluLeuLeuSerProGlyAsnPr 164
513 GAGAGGAGCCTTCTGTCGAGAGAAAGTGAACACAGAAAGTCTACT 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
164 oGlnGlyAlaPheLeuIleArgIleSerGluTyrThrLysGlyAlaLys 181
563 GCCTCTAGTGTGACTTGCAGAACGCCAAGGCGCTCAAGCTGAGAACAC 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 erLeuSerIleArgAspTrpAspGlnThrArgGlyAspHisValLysHis 197
613 TACAAATCCGCAAGCTGACAGCGGCGCTTCTACATCACTCCCGCAC 662
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
198 TyrLysIleArgLysLeuAspMetGlyLysTyrIleThrThrArgVal 214
663 CCAAGTTCACAGCCTGACAGAGCTGTGGCGCTACTACTCCAAACAGCGC 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 IGlPheAsnSerValGlnGluLeuValGlnHisTyrMetGluValAsnA 231
713 ATGGCTGTCCACCGCTCACCACCGTGTGCGCCACGCTCCAGCCGCGAG 762
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
231 spGlyLeuCysAsnLeuLeuIleAlaProCysThrIleMetLysProGln 247
763 ACTCAGGCGCTGGCCAGAGATGCCGTGGAGATCCCTCGGAGTGCCTGCG 812
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 ThrLeuGlyLeuAlaLysAspAlaTrpGluIleSerArgSerSerIleTh 264
813 GCTGAGAGTACAGTGGCGCCAGGCGCTTGGGAGGTGTGATGGAGA 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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264 rLeuGluAlaArgLysLeuGlyThrGlyCysPheGlyAspValTrpLeuGlyTr 281
863 CCTGGAACGGTATCCACAGAGGTGGCCATCAAAACCTGAGAGCTGGACG 912
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
281 hTrpAsnGlySerThrLysValAlaValLysThrLeuLysProGlyThr 297
913 ATGTCTCCAGAGCCTTCTCCAGAGAGGCCCGCAGTCAATGAGAGCTGAG 962
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
298 MetSerProLysAlaPheLeuGluGluAlaGlnValMetLysLeuLeuArg 314
963 GCATGAGAAAGCTGGTGCAGATTGTATGCTGTGTTTCAGAGAGCCCATTT 1012
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
314 gHisAspLysLeuValGlnLeuTyrAlaValAlaValSerGluGluProIle 331
1013 ACATCGTCACGAGATGATGAGCAAGGGGAGTGTCTGAGACTTCTTCAG 1062
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 yTlleValThrGluPheMetCysHisGlySerLeuLeuAspPheLeuLys 347
1063 GGGGAGACAGGCCAATFACCTCGCGCTGCTCAGCTGATGAGATGAGCTGC 1112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
348 AsnProGluGlyGlnAspLeuAlaArgLeuProGlnLeuValAspMetAla 364
1113 TCAGATCCCTTCAGGCAATGGCGTACGTGAGCGGATGAATACGTCCACC 1162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
364 aGlnValAlaGluGluMetAlaTyrMetGluArgMetAsnTyrIleHisA 381
1163 GGGACCTTCGTGCAGCCCAACATCCGTGGGAGAGAACCTGCTGGCAAA 1212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 rGAspLeuAlaArgAlaAlaAsnIleLeuValGlyGluArgLeuAlaCysLys 397
1213 GTGGCCGCACTTGGCGCTGCTGCGCTCATTTGAAGCAATGACTACAGCGC 1262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
398 lIleAlaAspPheGlyLeuAlaArgLeuIleLysAspAspGluTyrAsnPr 414
1263 GCGGCAAGGTCCAAATTCGCCATCAAGTGAAGCGCTCCAGAGCTGCC 1312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
414 oCysGlnIleLysLysPheProIleLysTrpThrAlaProGluAlaAla 431
1313 TCTATGCCGCTTACCATCAAGTGGACGTGTGCTTGGGATCCTG 1362
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 eupHeGlyArgPheThrIleLysSerAspValTrpSerPheGlyIleLeu 447
1363 CTGACTGAGCTCACACAAAGGAGCGGTCCTCCCTGCGGATGTGTA 1412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
448 LeuThrGluLeuIleThrLysGlyArgIleProTyrProGlyMetAsnLys 464
1413 CCGGAGGCTGCTGACACAGTGAAGCGGGCTACCGGATGCCCTGCCCGC 1462
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
464 sArgGluValLeuGluGlnValGluGlnGlyThrHisMetProCysProP 481
1463 CGAGGTGCCGAGTCCCTGCACGACCTCATGTATGCCAGTGTGGCGGAG 1512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 roGlyCysProAlaSerLeuTyrGluAlaMetGluGlnThrTrpArgLeu 497
1513 GAGCTGAGAGAGCGGCCACCTTCGATGACTGACGAGCCTTCTGAGAGA 1562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
498 AspProGluGluArgProThrPheGluTyrLeuGlnSerPheLeuGluAs 514
1563 CTACTTCAGTCCACGAGCCCATACAGCCCGGGGAG 1602
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
514 pTyrPheThrSerAlaGluProGlnTyrGlnProGlyAsp 527

```


XX 28-MAY-1999; 99MO-US11780.
XX
XX 29-MAY-1998; 98US-0087220.
XX

(SCRI) SCRIPPS RES INST.

PI Cheresch DA, Elliceiri B, Schwartzberg PL;

XX WPI; 2000-116335/10.
XX N-PSDB; AA229700.
XX

PT Using tyrosine kinase Src for modulating angiogenesis in tissues useful
in, e.g. treatment of chronic articular rheumatism -
PS Claim 1; Fig 2; 80pp; English.

XX The present sequence is the wild-type chicken c-Src tyrosine kinase.
This Src protein can be used to modulate angiogenesis. When the Src
protein is inactivated, angiogenesis is inhibited while, when it is
activated, angiogenesis is potentiated. The modified or variant Src can
be used to treat inflammatory diseases like, arthritis, rheumatoid
arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer
associated disorders.

XX Sequence 533 AA;

alignment_scores:

Quality: 2663.50 Length: 536
Ratio: 5.112 Gaps: 1
Percent Similarity: 97.201 Percent Identity: 94.030

alignment_block:

US-09-444-711-1 x AAAY44447 ..

Align seg 1/1 to: AAAY44447 from: 1 to: 533

1 ATGGTTCACACAGACAGACAGCCAGATGCCAGCCAGCGCGCGCG 50
1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgLys 17
51 CCTGAGCGCGCGCGAGACGTCGACGCGCGCGCGCGCGCGCGCG 100
17 IleuGlnProProAspSerThrHis.....HisGlyGlyProPro 31
101 CCTGCAGACCGCCGAGACAGCCAGCGCGCGCGCGCGCGCGCG 150
31 AsnGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47
151 AGCG 200
48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGly 64
201 CAATCTCTCGACACCGTCACCTCCCGCGAGAGCGCGCGCGCGCG 250
64 AsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeu 81
251 GTGGAGTGCACACCTTGTGGCGCTTATGACATAGTACTAGAGG 300
81 LysIleValThrThrPheValAlaLeuThrAspTyrGluSerArgThr 97
301 ACAGACCTCTCTCAGAAAGCGAGCGCGCGCGCGCGCGCGCGCG 350
98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsn 114
351 GGAGGAGACGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 400
114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrGlnGlnThrGly 131
401 ACATCCCGACCACTACGTGGCGCGCGCGCGCGCGCGCGCGCG 450
131 yTrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGlu 147

451 TGGTATTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTG 500
148 TrpTyrPheGlyLysIleThrArgArgGlnSerGlnArgLeuLeu 164
501 TGCAGACACCGCGAGAGGACCTCTCTGTCGAGAAAGTGAGAC 550
164 nProGlnAsnProArgGlyThrPheLeuValArgGlnSerGlnThr 181
551 AAGGTGCTTACTGCTCTCAGGTGTGACTGTGACAAACGCGAGG 600
181 yGlyAlaTyrCysLeuSerValSerAspPheAsnAlaLysGly 197
601 AAGGTGAGACATACAGATCCGACAGCGCGCGCGCGCGCGCG 650
198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPhe 214
651 CACCTCCCGCACCCAGTTCACAGACCTGACAGCAGCTGGTGGCT 700
214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyr 231
701 CCAACACCGCGATGCGCTGTGCGACCGCTCACACCGGTGGCC 750
231 eLysHisAlaAspGlyLeuGlnHisArgLeuThrAsnValLysPro 247
751 TCCAGCGCGGACACTCAGGCGCGCGCGCGCGCGCGCGCGCG 800
248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGlnIle 264
801 GGAATGCTGCGCGGTGAGGTCAGAGTCAGCGCGCGCGCGCGCG 850
264 gGluSerLeuArgLeuGlnValLysLeuGlnGlnCysPheGlyGlu 281
851 TGTGATGGGACCTGAGACGATACACAGGTCGCGCGCGCGCG 900
281 aLTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLys 297
901 AAGCTGCGACAGATGCTCCAGAGCGCTTCTGACAGGCGCGCG 950
298 LysProGlyThrMetSerProGlnAlaPheLeuGlnGlnAlaGln 314
951 GAAGAAGCTGAGGATGAGAGCGTGGCAGTGTGATGCTGGT 1000
314 tLysLysLeuArgHisGlnLysLeuValGlnLeuTyrAlaValSer 331
1001 AGGACCGCATTTACATGTCACGAGTACATGACAGGAGGATG 1050
331 LngLuproIleTyrIleValThrGlnLysMetSerLysGlySer 347
1051 GACTTTCTCAAGGGGAGACAGGACAGTACCTGGCGCTGCTC 1100
348 AspPheLeuLysGlyGlnMetGlyLysTyrLeuArgLeuProGln 364
1101 GGACATGCTGCTCAGATCGCTTCAAGGATGGCTAGCTGAGCG 1150
364 LAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGln 381
1151 ACTAGTGCACCGGACCTTGTGCGAGCAGACATCTGGTGGAG 1200
381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGly 397
1201 CTGGTGTGCAAGTGGCGGACTTGGGCTGGCTGGCTCATGAG 1250
398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGlu 414
1251 TGAGTACAGCGCGCGCGAGGTGCCAAATTCCTCCATCAAGTG 1300
414 nGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrp 431
1301 CAGAAAGCGCGCTTATGCGCGCGCTTACACATCAAGTGGAG 1350
431 rGlnAlaAlaLeuTyrIleArgPheMetIleLysSerAspValTrp 447

601 AACGTGAAGACCTACAGATCCGACAGCTGACAGCGCGGCTTACAT 650
 198 AsnVallyshistyllysilearglylsleuaspserglyglyphenyl 214
 651 CACCTCCCGCACCCAGTTCAACAGCCTGACAGAGCTGGTGGCTTACT 700
 214 ethserargthrghlnpheserSerleuclnglnleuValAlaIatyr 231
 701 CCAACACAGCGCATGGCGCTGTCACCGCTCCACACAGCTGGCGCCAG 750
 231 erlyshisAlaspolyLeucysHisArgleuthrAsnValysProthr 247
 751 TCACAGCCGACAGACTCAGAGCGCTGGCCACAGATGCTGGAGATCCCTG 800
 248 SerlysproglnthrGlnglyleuAlalysaspAlatrpGlnleprolr 264
 801 GGAGTCGCTGGCGCTGAGAGTCAAGCTGGCCAGGCGCTGTTGGCGAG 850
 264 ggluserleuargleugluVallylsleuclnglnlycyspheglyglu 281
 851 TGTGATGGGACCTGGAACGCTTACCACAGGCTGGCCATCAAAACCTG 900
 281 altrpMeGlythrtrpasnnglythrArgValAlalleusthrleu 297
 901 AAGCTGACAGATGTCACAGAGCGCTTCGACAGAGGCCAGGTCAT 950
 298 LysproglythrMetSerProgluAlapheleuglnleuAlaValme 314
 951 GAAGAACCTGAGGATGAGAACCTGTCAGATGATGCTGATGCTGTTGAG 1000
 314 tlystysleuarghlsGlylsleuValGlnleuValAlaValSerG 331
 1001 AGAGCCCATTTACATCGTACAGAGTACATAGACAAGGGAGTTGCTG 1050
 331 lngluProiletyrileValthrGluTyrMetSerlysglyserleu 347
 1051 GACTTTCACAGAGGGGACAGGACAGTACCTGGCTGCTCAGCTGCT 1100
 348 AspPheleuLysGlylMetGlyltyrleuArgleuProgluLeuVal 364
 1101 GGACATGGCTGCTGATGCTGACGCTGACGCTGCTGACGCTGATG 1150
 364 lAspMetAlaAlaGlnleuAlaSerGlyMetAlaItyrValGluArg 381
 1151 ACTAGCTCCACCGGACCTTCGTCAGCCACATCCTGGTGGAGAGAAC 1200
 381 sotyrValHisArgspLeuArgAlaAlaAsnIleleuValGlyluasn 397
 1201 CTGGTGTCAAGTGGCGGACCTTGGGCTGGCTGGCTGATGAGACAA 1250
 398 leuValCysLysValAlaAspPheGlyleuAlaArgleuIleGluasp 414
 1251 TGAGTACAGGGGGCGCAAGTGGCCAAATTGCCATCAAGTGGAGGCTC 1300
 414 ngluTyrThrAlaArgGlnGlyAlaLysPheProIlelystrPthAla 431
 1301 CAGAAGTGCCTCTTATGGCGCTTACCATCAAGTCGAGCTGTGGTCC 1350
 431 rogluAlaAlaLeuTyrGlyArgPheThrIleLysSeraspAlatrpser 447
 1351 TTCGGAGATCTGCTGACGTGACGTCAACACAAAGGAGCGGCTGCTACCC 1400
 448 PheGlyIleleuLeuThrGlnleuThrThrLysGlyArgValProtyrPr 464
 1401 TGGATGGTGAACCGGAGGTGCTGGACAGGTCGAGCGGGCTACCGGA 1450
 464 OGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArg 481
 1451 TGCCCTGGCCGCGGAGTGTCCGAGTCCCTGACAGACCTCATGTGCCAG 1500
 481 etProCyProProglucysProgluserLeuHisaspLeuMetCysGln 497

1501 TGCTGGCGGAAGAGACCTGAGAGCGGCGCCACCTTCGATGACTGCAAGC 1550
 498 CysTrpArgargaspProgluArgProThrPheGluTyrleuGlnAl 514
 1551 CTTCCTGGAGACTACTTACGTCACCGGAGCCCATACAGCCCGGGG 1600
 514 aPheleuGluAspTyrPheThrSerThrGluProgluTyrGlnProgl 531
 1601 AGAACCTC 1608
 531 luanleu 533

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AAV44449

seq_documentation_block:
 ID AAV44449 standard: Protein: 533 AA.

AAV44449;
 22-MAR-2000 (first entry)

DE Mutant chicken c-*Src* tyrosine kinase, *SrcA*.

XX Angiogenesis; tyrosine kinase; *Src*; inhibition; activation; modulate;
 KM chicken; mutant *Src*; *SrcA*; point mutation; Y527F; phosphorylation;
 KM negative regulation; tyrosine; inflammatory disease; osteoporosis;
 KM rheumatoid arthritis; diabetic retinopathy; restenosis; cancer.

XX *Gallus* sp.
 OS Synthetic.

XX Key location/Qualifiers

FT Misc-difference 527 /label= Y527F
 FT /note= "Wild type Tyr replaced with Phe"

PN W09961590-A1.

XX 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11780.

PR 29-MAY-1998; 98US-0087220.

XX (SCRI) SCRIPPS RES INST.

PA Cheresch DA, Elliceiri B, Schwartzberg PL.

XX WPI: 2000-116335/10.

DR Using tyrosine kinase *Src* for modulating angiogenesis in tissues useful

PT in, e.g. treatment of chronic articular rheumatism -

XX Claim 3; Page -: 80pp; English.

XX The present sequence is the mutant chicken c-*Src* tyrosine kinase,
 CC *SrcA*. This sequence has a point mutation, Y527F, to activate c-*Src*.

CC This site is involved in negative regulation by the kinase *CSK*.
 CC Phosphorylation of Tyr residue at 527 inactivates the protein. But in
 CC the mutated *SrcA*, the regulatory Tyr is replaced with Phe, thus
 CC constitutively activating the protein. This mutant *Src* protein can be
 CC used to modulate angiogenesis. When the *Src* protein is inactivated,
 CC angiogenesis is inhibited while, when it is activated, angiogenesis is
 CC potentiated. The mutant or variant *Src* can be used to treat inflammatory
 CC diseases like: arthritis, rheumatoid arthritis, diabetic retinopathy,
 CC restenosis, osteoporosis and cancer associated disorders.
 CC Note: This sequence is not found in the specification, but derived
 CC from the sequence in Fig 2.

CC Sequence 533 AA;

alignment_scores:

AC AAR39705;
 XX 23-DEC-1993 (first entry)
 XX
 DE Chicken pp60 c-src protein.
 XX
 KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
 XX
 OS Gallus gallus.
 XX
 PN MO9314193-A.
 XX
 PD 22-JUL-1993.
 XX
 PF 05-JAN-1993; 93MO-US00445.
 XX
 PR 06-JAN-1992; 92US-0820011.
 XX
 (UYVA) UNIV YALE.
 XX
 PI Bell L, Luthringer DJ, Madri JA, Warren SL;
 XX
 DR WPJ; 1993-243209/30.
 XX
 DR P-PSDB; AAR39705.
 XX
 XX Genetically engineered endothelial cells - which exhibit enhanced
 PT cell migration, urokinase-type plasminogen activator activity,
 PT and reduced mononuclear cell adhesion and fibronectin prodn
 PT
 PS Disclosure; Page 64-66; 91pp; English.
 XX
 XX The DNA encoding a portion or (more preferably) the entire pp60
 CC c-src polypeptide (given in AAQ46687) is used to transform endothelial
 CC cells. Transformed cells produce increased amounts of pp60 c-src and
 CC have improved therapeutic properties. They migrate at faster rates
 CC than non-transformed counterparts; have an enhanced ability to
 CC inhibit the formation of thrombi and/or dissolve thrombi once they
 CC have formed and exhibit reduced mononuclear cell adhesion. They can
 CC also be used to improve the success of surgical procedures such as
 CC coronary angioplasty, heart bypass surgery, vessel graft and stent
 CC implantation.
 CC
 SQ Sequence 533 AA;
 Alignment_scores: Quality: 2658.50 Length: 536
 Ratio: 5.103 Gaps: 1
 Percent Similarity: 97.201 Percent Identity: 93.843
 Alignment_block:
 US-09-444-711-1 x AAR39705 ..
 Align seg 1/1 to: AAR39705 from: 1 to: 533

64 easnThrSerAspThrValThrSerProGlnArgAlaLeuAlaG 81
 251 GTGAGTGCACACCTTTGGCCCTGATGACTATAGTCTAGACGAG 300
 81 LylValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97
 301 ACAGACCTTCCTTCAGAAAGGCGGCGCTCCACATTGTCAACAAC 350
 98 ThrAspLeuSerPheLysLysGluArgLeuGlnLeuAlaLysnTh 114
 351 GGAGGAGACGTGTGGCTGGCCACTCGCTGACACAGACAGACAGCT 400
 114 rGlLysAspTrpTrpLeuAlaHisSerLeuThrGlnGlnThrGlyT 131
 401 ACATCCCGACGACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAG 450
 131 YrLeProSerAsnTyrValAlaProSerAspSerIleGlnIleGlu 147
 451 TGGTATTTTGGCAAGATCACAGACGGAGTGCAGAGGCTTACTGCTCA 500
 148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeu 164
 501 TGCAGAGAACCCGAGAGGAGACCTCCTCGTGAGAAAGTAGACACGA 550
 164 nProGlnAsnProAlaGlyThrPheLeuValArgGluSerGlnThrTh 181
 551 AAGGTGCTACTGCTCTGCTGAGTGTGACTTCGACACAGCCAGGCTC 600
 181 YsGlyAlaTyrCysLeuSerValSerAspPheAsnAlaLysGlyLeu 197
 601 AACGTGAGACACTACAAAGATCCGCAAGCTGGACAGCGGCGCTTCAC 650
 198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyLysPheYr 214
 651 CACCTCCCGCCACCGATTACACAGCTGCAGAGCGTGGGCGCTACTAC 700
 214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrLys 231
 701 CCAACACGCGCATGAGCTGTGTCACACCGCTGACACAGCTGCGCCAC 750
 231 eLysHisAlaLysArgLysLeuGlnLysArgLeuThrAsnValCysPro 247
 751 TCCAAAGCCGACAGCTCAGGCGCTGGCCAGAGATCCCTGGAGATCC 800
 248 SerLysProGlnThrGlnLysLeuAlaLysAspAlaTrpGlnLeuPro 264
 801 GGAGTGGCTGGCGGTGAGGATGAGGCGGCGGCTGCTGGGAGAG 850
 264 GlnSerLeuArgLeuGlnValLysLeuGlnGlnGlyCysPheGlyGlu 281
 851 TGTGATGGGAGCTGGAAGGCTGACACAGGAGGTGGCAAAACCCCTG 900
 281 aTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297
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 298 LysProGlnLysAsnMetSerProGlnAlaPheLeuGlnGlnAlaGln 314
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531 lAsnLeu 533

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ID ABG23778 standard: Protein: 565 AA.
XX ABG23778;
AC
XX
XX
DT 18-FEB-2002 (first entry)
XX
XX
DE Novel human diagnostic protein #23769.
XX
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang Yr.
XX
DR N-PsDB; AAS87965.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20: SEQ ID No 54137; 103pp: English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting and
CC quantitating a polypeptide in tissue, as molecular weight markers or as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating

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ID ABG23777 standard; Protein: 351 AA.
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ABG23777:
X.
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23768.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
N-PsDB; AAS87964.
XX

```

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX
XX Claim 20; SEQ ID NO 54136; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WPIO
CC at ftp.wipo.int/pub/published_pct_sequences.

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XX Sequence 351 AA:

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 Ratio: 5.319
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-444-711-1 x ABG23777 ..

Align seg 1/1 to: ABG23777 from: 1 to: 351

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472 oThrPheGluIlyrLeuGlnSerIleLeuGlnAspPhePheThrAlaThrG 489
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489 IuThrGlnIlyrGln 493
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CC treatment and modulation of diseases, disease symptoms or the effect of
 CC other physiological events mediated by kinases, having one or more kinase
 CC enzymes involved in their pathology.
 XX

SO Sequence 508 AA:

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Quality: 1464.00 Length: 454
 Ratio: 3.812 Gaps: 3
 Percent Similarity: 84.581 Percent Identity: 59.912

alignment_block:

US-09-444-711-1 x AAB37700 ..

Align seg 1/1 to: AAB37700 from: 1 to: 508

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88 rGleLeuGlnGlnSer...GlyGluTrpTrpLysAlaGlnSerLeuThr 103
385 ACAGAGACAGACAGATACATCCCAAGCACTAGTGGCCCTCCGACTC 434
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453 GluArgGlyTyrlArgMetValArgProAspAsnGlyProGlnGluLeuTy 469
1485 CGACCTCATGTGCCAGTGTGGCGGAAAGAGCTGAGAGCGGCCACCT 1534
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469 rGlnLeuMetArgLeuGlySerTrpLysGlnArgProGlnAspArgProThr 486
1535 TCGAGTACCTGCGAGCGCTTCCTGAGAGACTACACTCAGTCCACGAGCC 1584
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486 heAspTyrlLeuArgSerValLeuGlnAspPhePheThrAlaThrGlnGly 502
1585 CAGTACAGGCC 1596
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503 GlnTyrlGlnPro 506
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seq_documentation_block:
ID: AAV49420 standard; Protein: 509 AA.
XX
AC AAV49420;
XX
DF 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family.
OS Homo sapiens.

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151 egllylsleuglyarplysaspalaglualrglnleuleuserphecilya 168
509 ACCGAGAGAGGACCTTCTCTGCGAGAAAGTGAACACGAGAAAGTCC 558
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609 GCACATCAAAATCCGCAAGCTGGACAGCGGCGCTTACATCACTCC 658
201 shstlyrlyleleargplysleuaspanglyltyrtyrlethrtha 218
659 GCACCCGCTCAACAGCGCTGAGACGTGGGCGCTACTACTCAACAC 708
218 rgalaglnphegluthrleuglnleuvalglnhstysrsergluarg 234
709 GCCGATGCGCTGTGACCCGCTCACCGCTGCGCCACGCTCAAGCC 758
235 Alalaglyleucysylargleuvalvalprocyshstlysglymetpr 251
759 GCAGACTCAGCGCGCTGCC.....AAGATGCGCTGGAGATCCCTC 799
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800 GCGAGTGCCTGCGCGCTGAGGTCAAGTGGCGCGCTGCTTTGGCGAG 849
268 rgluserleuglnleulellysarpleuglyasnlglnpheglyglu 284
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1300 CCAGAGAGTGGCGCTTATGGCGCTTACCATACATCAAGTCGAGCGTGTGCT 1349
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1400 CTGGGATGTGAACCGGAGGTGCTGACACGAGCTGAGCGGGCGCTACCGG 1449
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1450 AMGCCGTCGCCCGCGAGAGTGTCCGAGTCCCGTGCAGACCTCATGTGCA 1499
485 MetprocyssproglinspocysprolleserleuHlsGluLeuMetleHl 501
1500 GTGCTGGCGGAAGAGAGCTGAGAGAGCGGCCACCTTCGATGACTGCGAC 1549
501 scystyrlystysaspProglugluargProthrphleglutyrlleugl 518
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seq_documentation_block:
; Sequence 15, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizky, Mikhail
; APPLICANT: Sures, Itman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; City: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: No. 6326469e
; US-08-426-509A-15

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alignment_scores:
Quality: 1856.00      Length: 530
Ratio: 4.171          Gaps: 3

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151 AGGGGGGCGCTTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 200
    |||
51  SerAlaIaIaheAlaProAlaIaIaIaGluProLysLeuPheGlyGlyPh 67
201 CAATCCTCGGACACGCTCACTCCCGACGAGGGCGCGCGCGCGCGCG 250
    |||
67  eaAnSerSerAspThrValThrSerProGlnArgAlaGlyProLeuIaG 84
251 GTGAGTACGACACCTTTGTGGCCCTATGACTATGAGTCTAGAGGAG 300
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301 ACAGACCTGTCTTCAAGAAAGCGGAGCGGCTCCAGATTGTCAACAAC 350
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101 ThrAspLeuSerPheLysGlyGluArgLeuGlnIleValaAsnAsnTh 117
351 GGAGGGAGATGCGTGGCGCCCACTGCTCAGACAGACAGACAGAGCT 400
    |||
117 rGluGlyAspTrpTrpLeuAlaHisSerLeuSerThrGlyGlnThrGly 134
401 ACATCCCGACCACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAG 450
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134 yrlLeProSerAsnIyrValAlaProSerAspSerIleGlnAlaGluGlu 150
451 TGGTATTTTGGCAAGATCACACAGCGGAGTCAAGCGGTACTGTCAA 500
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151 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuAs 167
501 TCGAGAGAACCCGAGAGGACCTTCTCGTGGCGAAAGTGAACAACA 550
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701 CCNAACACCGCGATGGCTGTGGCACCGGCTCCACACCGTGGCCGAC 750
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751 TCCAGCCCGACAGCTCAGGGCTGCGCAAGAGATGCTGGAGATCCCTCG 800
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801 GGAGTGGCGCGGCTGGAGGTCAAGCTGGGCGCAGGGCTGTTGGCGAG 850
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267 gEusSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGly 284
851 TGTGATGGGACCTGGAACGGTACACACAGGGTGGCATCAAAACCTG 900
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901 AAGCTGGACAGATGTCTCCAGAGCCCTTCTCAGAGGCGCCAGGTGAT 950
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301 LysProGlyThrMetSerProGlnAlaPheLeuGlnGluIaGlnValMe 317
951 GAAGAAGCTGAGGATGAGAAAGCTGGTGCAGTTGTAATGCTGTGTTTCA 1000
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317 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValaValSerG 334

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351 AspPheLeuLysGlyGluThrGlyLysTyrLeuArgLeuProGlnLeuVal 367
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367 lAspMetAlaIaGlnIleAlaSerGlyMetAlaTyrValGluArgMetAla 384
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384 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 400
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434 rGluAlaAlaLeuIyrTylArgPheThrIleLysSerAspAlaTrpSer 450
1351 TTCGGGATTCGTGACTGAGCTCACACAAAGGAGCGGTGCCCCCTACCC 1400
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1401 TGGATGGTGAACCGGAGGTGCTGGACAGGTGAGCGGGGCTACCGGA 1450
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XX   AAV44447;
AC   AC
XX   AC
DT   22-MAR-2000 (first entry)
DE   Wild-type chicken c-src tyrosine kinase.
KW   Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW   chicken; viral expression vector; replication competent; variant Src;
KW   inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW   diabetic retinopathy; osteoporosis; cancer.
OS   Gallus sp.
XX   XX
XX   WO9961590-A1.
XX   PN
XX   PD   02-DEC-1999.

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Ratio: 5.105 Gaps: 1
Percent Similarity: 97.201 Percent Identity: 93.843

Alignment block:

US-09-444-711-1 x AAY44449

Align seg 1/1 to: AAY44449 from: 1 to: 533

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51  CCTGAGCGCCCGGAGAACGTGACAGCGCGCTGCGCGGCGGCTTCCCG 100
|||||
17  rLeuLupProAspSerThrHis.....HisGlyGlyPhePro 31
|||||
101  CCTGCGACAGCCCGACAGACCGCTGCGCGGCGGCGGCGGCGGCGG 150
|||||
31  lAserGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47
|||||
151  AGCGGGCGCTTGGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 200
|||||
48  SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64
|||||
201  CAATCTCTCGACACCGTCACCTCCCGGAGAGGGGCGGCGGCGGCGG 250
|||||
64  eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaAlaG 81
|||||
251  GTGAGTAGCACACTTGTGGCCCTCTATGACTATGAGTCTAGAGAGAG 300
|||||
81  LylGlyValThrThrPheValAlaLeuTyAspTyrGluSerArgThrGlu 97
|||||
301  ACAGACCTGCTCTTCAAGAAAGCGAGCGGCTCCAGATTGTCACACAC 350
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98  ThrAspLeuSerPheLysLysGlyLysArgLeuGlnLleValAlaAsn 114
|||||
351  GGAGGAGACATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 400
|||||
114  rGluGlyAspTyrPheLysAlaHisSerLeuThrThrGlyGlnThrGly 131
|||||
401  ACATCCCGACAGACTACGTGGCGGCGGCGGCGGCGGCGGCGGCGG 450
|||||
131  YrLleProSerAsnTyrValAlaProSerAspSerLleGlnAlaGluGlu 147
|||||
451  TGGATTTTGGCAGATCACACAGAGGAGTCAAGAGCGGTACTGCTCAA 500
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148  TrpTyrPheGlyLysLleThrArgArgGluSerGluArgLeuLeuAsn 164
|||||
501  TGCAGAGAACCGAGAGGAGGACTCTCGTGGGAGAAAGTGAGACACGA 550
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164  nProGluAsnProArgGlyThrPheLeuValAlaGluSerGluThrThrL 181
|||||
551  AAGGTGCTACTGCTCTCAGTGTGTGACTTCGACACGCAAGGCGCTC 600
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181  YsGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197
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601  AACGTGAAGCACTACAGATCCGCAAGCTGACACGCGGCGGCTTACAT 650
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198  AsnAlaLysHisTyrLysLleArgLysLeuAspSerGlyGlyPheTyrL 214
|||||
651  CACTCCCGGACCCAGTCAACAGCGCTGACAGCGTGTGGCTTACTACT 700
|||||
214  eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231
|||||
701  CCAAGACAGCGGATGGCTGTGCCAGCGCTCACACCGGTGGCGCCACG 750
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231  eTrLysHisAlaAspLysLeuLysSerArgLeuThrAsnValCysProThr 247
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751  TCCAGGCGGACAGACTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 800
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248  SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTyrGluLleProAr 264
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851  TGTGATGGGAGCCTGGAAGGTATCACACAGGAGGGGCGGCAAAACCTG 900
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281  aTrpMetGlyThrTyrAsnGlyThrThrArgValAlaLleLysThrLeu 297
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901  AAGCTTGGACAGATGTCTCCAGAGGCTTCTGACGAGGCGGCGGCGAT 950
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314  tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValAlaSer 331
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331  lndLuproLleTyrLleValThrGluTyrMetSerLysGlySerLeuLeu 347
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348  AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364
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1101  GGCATGGCTGCTCAGATGCGCTCAGGCAATGGCGTACGTGAGCGGATGA 1150
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364  lAspMetAlaAlaGlnLleAlaSerGlyMetAlaTyrValGluArgMeta 381
|||||
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398  LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuLleGluAspAs 414
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1251  TGGATACAGGCGGCGGCGGCAAGGCTCCAAATTCCTCATCACTGAGGCTC 1300
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414  nGluTyrThrAlaArgGlnGlyAlaLysPheProLleLysTyrPheAla 431
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1451  TGGCCGTGCGCGGCGGAGTGTCCGAGTCCCTGACAGACCTCAAGTCCAC 1500
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481  eCProLysProProGluLysProGluSerLeuHisAspLeuMetCysGln 497
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498  CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514
|||||
1551  CTTCCTGGAAGACTACTTACGTCCACCGAGGCGGCGGCGGCGGCGG 1600
|||||
514  aPheLeuGluAspTyrPheThrSerThrGluProGlnPheGlnProGlyG 531
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ID AAR39705 standard; Protein: 533 AA.
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398 LeuValcYglvYsValAlAsrPheglYleuAlArGleuIleGluAspAs	414
1251 TAGAGTCAGGGCGGGGCAAGGTGCCAAATTCCTCAATGAGTGAGGCTC	1300
414 nGtUtYtTlAlArGlnGlnIyAlArPheRtoIleYsSerSPrAlTtPsr	431
1301 CAGAACTCCCTCTATGGCGGCTTCACATGAAAGCGGAGCTGGTGC	1350
431 rGclAlAlAlArLeuYtGtIyArPheTtIleYsSerSPrAlTtPsr	447
1351 TTCGGAGTCTGTGTAGTGTCAACACAAAGGAGGAGTGCCTTACC	1400
448 PheGtIleleuIleuThrGtIleuThrIlySgIyArGValrProtYtGr	464
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498 CysTrPrArGArGAsrPrGtIyGlnArGrOtIhPrheGtIyTtYleuGlnAl	514
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XX AAV44451;	
XX 22-MAR-2000 (first entry)	
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XX Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;	
XX chicken; mutant; Src(K295M); point mutation; tumor cell signaling;	
XX ATP binding; proliferation; kinase domain; inflammatory disease; cancer	
XX osteoporosis; rheumatoid arthritis; diabetic retinopathy; restenosis.	
XX Galius sp.	
XX Synthetic.	
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XX /label= K295M	
XX /note="Wild type Lys replaced with Met"	
XX W09961590-A1.	
XX 02-DEC-1999.	
XX 28-MAY-1999; 99MO-US11780.	
XX 29-MAY-1998; 98US-0087220.	
XX	

(SCRI) SCRIpps RES INST.
Cheresh DA, Eliceiri B, Schwartzberg PL;
WPI; 2000-116335/10.

using tyrosine kinase Src for modulating angiogenesis in tissues useful
in, e.g. treatment of chronic articular rheumatism -

Claim 6; Page -: 80pp; English.

The present sequence is the mutant chicken c-Src tyrosine kinase,
Src(K295M). This sequence has a point mutation, K295M, in the kinase
domain, which prevents ATP binding and also blocks kinase dependent
src functions related to vascular cell and tumour cell signalling and
proliferation. This mutant Src(K295M) protein, can be used to modulate
specifically inhibit angiogenesis. When the Src protein is inactivated,
angiogenesis is inhibited while, when it is activated, angiogenesis is
potentiated. The mutant or variant Src can be used to treat inflammatory
diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy,
restenosis, osteoporosis and cancer associated disorders.

Note: This sequence is not found in the specification, but derived
from the sequence in Fig 2.

alignment_scores:	quality: 2657.50	length: 5366
	ratio: 5.111	gaps: 1
Percent Similarity:	97.015	Percent Identity: 93.843

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US-09-444-711-1 x AAAY44451 ..
Align seg 1/1 to: AAAY4451 from: 1 to: 533
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 1551 CTTCCTGGAGGACTACTCAGCTCCAGCCAGGCGCCAGTACCAGCCCGGG 1600
 |||||.....
 514 aPheLeuGlnAsPryrPheTrISerThGlnProGlnuTyGInProGlyG 531
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 1601 AGAACCTC 1608
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 531 IuASnIeu 533

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98 AlaLeuTyrAspTyrGlnAlaArgThrGluAspLeuSerPheLys 114
321 AGCGAGCGGCTCCAGATGTGCAACAGAGGAGGAGACTGGCGGTG 370
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114 SgLYgluArgPheGlnIleIleAsnThrGluGlyAspTrpIleVal 131
371 CCCACTCGCTCAGCAGAGAGAGAGAGGCTACATCCACAGACTACGTG 420
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131 laArgSerIleAlaThrGlyLysAsnGlyTrpIleProSerAsnTyrVal 147
421 GCGCCCTCCGACTCCATCCAGGCTGAGAGAGTGTATTTGGCAAGATCAC 470
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148 AlaProAlaAspSerIleGlnAlaGlnGluTrpTyrPheGlyLysMetG1 164
471 CAGACGGGAGTCAAGAGGGTTACTGCTCATGACAGAGAACCCGAGAGGA 520
164 YArgLYsAspAlaGlnArgLeuLeuAsnProGlyAsnGlnArgGlyI 181
521 CCTTCCTCGGCGAGAAAGTGAAGACAGAAAGGCTGCTGCTGCTCA 570
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181 lePheLeuValArgGluSerGluThrThrLysGlyAlaTyrSerLeuSer 197
571 GTGTCTGACTTCGACAAAGCCAAAGGCTCAAGCTGAAGACTACAAAGAT 620
198 IleArgAspTrpAspGlnIleArgGlyAspAsnValLysHisTyrLysI 214
621 CCGCAAGCTGGACAGCGGCGGCTTCACATCACCCTCCGACCCAGTCA 670
214 eArgLYsLeuAspAsnGlyIleTyrTrpIleThrArgAlaGlnPheA 231
671 ACAGCCTGCGAGAGCTGGTGGCTACTACTCAACACAGCGAGAGGCTG 720
231 sPThrLeuGlnLysLeuValLysHisTyrThrGlnHisAlaAspGlyLeu 247
721 TGGCACCGCTCACCACCGTGTGCCCCACGTCACAGCCGAGACTCAGGG 770
248 CysHisLysLeuThrThrValLysProThrValLysProGlnThrGlnG1 264
771 CCGGCGCAAGGATGCTGGGAGATCCCTCGGAGTGGCTGGCTGGAGG 820
264 YLeuAlaLYsAspAlaTrpGlnIleProArgLysSerLeuArgLeuLuv 281
821 TCAAGTGGGCGGAGGCTGCTGGGAGGAGTGGATGGGAGACTGGAAC 870
281 alLYsLeuGlnGlnLYsPheGlyGluValTrpMetGlyThrTrpAsn 297
871 GGTACCACAGGCGTGGCATCAAAACCTGAAGCCTGACGATGTCTCC 920
298 GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetMetPr 314
921 AGAGGCTTCCTGCAGAGAGGCCAGGCTCATGAAGAGCTGAGCATAGA 970
314 oGlnAlaPheLeuGlnGlnIleLysIleMetLYsLeuArgHisAspL 331
971 AGCTGTGACAGTGTATGCTGTGTTTCAAGAGGCCCATTTACATGTC 1020
331 YsLeuValProLeuTyrAlaValValSerGlnGluProIleTyrIleAl 347
1021 ACAGAGTACATGAGCAAGGAGGAGTTGCTGACTTCTCAAGGGGAGAG 1070
348 ThrGluPheMetSerLYsGlySerLeuLeuAspPheLeuLYsGluGlyAs 364
1071 AGGCAAGTACCTGCGGCTGCTCAAGCTGTTGGAGATGGCTGCATGAC 1120
364 pGlyLYsTyrLeuLYsLeuProGlnLeuValAspMetAlaAlaGlnIleA 381
1121 CCGCAGGAGATGGGCTAGTGGAGGAGGATGAAGTCCACCGGAGACTT 1170
381 laAspGlyMetAlaTyrIleGlnArgMetAsnTyrIleHisArgAspLeu 397
1171 CGTGCAAGCAATCCTGTGTGGAGAGAACCTGTGTCAAAAGTGGCGGA 1220
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398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLYsIleAlaAs 414
1221 CTTTGGCGCTGGCTGGCTCATTTGAAGACATGACAGAGCGGCGAG 1270
414 PheGlyLeuAlaArgLeuIleGlnAspAsnGlyLysThrAlaArgGln 431
1271 GTGCCAAATTCCTCATCAAGTGAAGCGGCTCCAGAAAGTGCCTCATGAC 1320
431 LYAlaLYsPheProIleLysTrpThrAlaProGlnAlaAlaLeuTyrGly 447
1321 CGCTTCACCATCAAGTGGAGCGTGTGCTTCCTGGGATCTGCTGACTCA 1370
448 ArgPheThrIleLYsSerAspValTrpSerPheGlyIleLeuGlnThrCl 464
1371 GCTCACCAAGAGGAGCGGCTGCTACCCGAGTGGATGGTGAACCGCGAG 1420
464 uLeuValThrLYsGlyArgValProTyrProGlyMetValAsnArgGluV 481
1421 TGCTGACACAGGTGGAGCGGCGCTACCGAGTGCCTGCGCGGAGTGT 1470
481 alLeuGlnGlnValGlnArgGlyTyrArgMetProCysProGlnGlyCys 497
1471 CCCAGTCTCTGCACAGACTCATGTGCCAGTGTGCGGAGAGACTCA 1520
498 ProGluSerLeuHisGlnLeuMetAsnLeuCysTrpLYsAspProAs 514
1521 GGAGCGGCGGCACTTCGAGTACTGACAGGCTTCTCTGAGAGACTACTCA 1570
514 pGluArgProThrPheGlyLysIleGlnSerPheLeuLysAspTyrPheT 531
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531 hAlaThrGlnProGlnTyrGlnProGlyGluAsnLeu 543
seq_name: /c9n2_6/prodata/1/1aa/6B_COMB.pep:US-08-426-509A-12
seq_documentation_block:
; Sequence 12, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Gillich, Axel
; APPLICANT: Glishizky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE


```

APPLICANT: United States of America
APPLICANT: Missenachafen E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
NUMBER OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-Apr-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-Apr-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

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alignment_scores:
Quality: 2834.00      Length: 536
Ratio: 5.287          Gaps: 0
Percent Similarity: 100.000  Percent Identity: 100.000

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Align seg 1/1 to: PCT-US95-05008-13 from: 1 to: 536

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17 TleuGluProAlaGluAsnValHisGlyAlaGlyGlyAlaPhePro 34
101 CCTGACAGCCCGGAGACGCGCGCGCGCGCGCGCGCGCGCG 150
34 laSerGlnThrProSerLysProAlaSerAlaAspLysHisArgGlyPro 50
151 AGCGGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCTT 200
51 SerAlaAlaPheAlaProAlaAlaAlaGluProLysLeuPheGlyGlyPh 67
201 CAACCTCCGCGACACCGTCACTCCCGCGAGAGCGCGCGCGCT 250

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251 GTGGAGTGACACCTTTGTGGCCCTCTATGACTATGCTTAGACGCGAG 300
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84 LylGlyValThrThrPheValAlaLeuLysArgPtyrGlnSerArgThrGlu 100
301 ACAGACTGTCCTTCAAGAAGCGGAGCGGCTCCAGTTGTCACAAACAC 350
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101 ThrAspLeuSerPheLysLysGlyLysArgLeuGlnLysValAsnThr 117
351 GGAGGAGAGACTGGCTGGCGCCGCGCTGCGACAGACAGACAGAGCT 400
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117 rGluGlyAspTrpTrpLeuAlaHisSerLeuSerThrGlyGlnThrGly 134
134 YrlleProSerAsnTyValAlaProSerAspSerIleGlnAlaGluGlu 150
401 ACATCCCGCAACACTACGTGGCGCGCTCGACACTCCATCCAGCTGAGAG 450
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451 TGCTATTTGGCAAGATCACACAGCGGAGTCAAGAGGCTTACTGCTCAA 500
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151 TrpTyPheGlyLysIleThrArgArgGluSerGluArgLeuLeuAs 167
501 TGCAGAGAACCCGAGAGGAGACTTCCCTGCGGAGAAAGTGAACACGA 550
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167 nAlaGluAsnProArgGlyThrPheLeuValArgLysSerGluThrThrL 184
551 AAGTGCTACTGCTCTCACTGCTGACTTGCACAACGCCAGAGGCGCTC 600
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184 YsgLysAlaTyrcysLeuSerValSerAspPheAspAlaLysGlyLeu 200
601 AACGTGAAGCACTACAAAGATCCGCAAGCTGGACAGCGCGCTTCTACAT 650
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201 AspValLysHisIleTyrcysLysIleArgLysLeuAspSerIleGlyPheTyrl 217
651 CACCTCCCGGACACGAGTTCACAGCCCTGACAGCACTGCTGCTTACTACT 700
|||||
217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaIleTyrcys 234
701 CCAACACGCGGATGGCTGTGCGACCGCTCACACCGTGTGCGCCAGC 750
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234 eLysHisAlaAspGlyLeuGlyHisArgLeuThrThrValcysProThr 250
751 TCCAGCGCGGAGACTCAGGCGCTGCGCAAGATCCCTGGAGATCCCTCG 800
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251 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 267
801 GGAATGCTGCGGCTGAGGTCAGAGCTGGCGCAGGCGCTTGGCGGAG 850
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267 gGluSerLeuArgLeuGlnValLysLeuGlyGlnGlyCysPheGlyGluV 284
851 TGTGATGGGAGCTTGAGACGGTACACAGGAGTGGCCATCAAAACCTG 900
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284 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 300
901 AAGCCTGGACAGATGCTCCAGAGGCTTCTGCGACAGGCGCCAGGTAT 950
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301 LysProGlyThrMetSerProGluAlaPheLeuGlnGlnAlaGlnValMe 317
951 GAAGAAGCTGAGGATGAGAAGCTGTGAGTTGATGCTGTTGTTGAG 1000
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317 TLysLysLeuArgHisGlnLysLysLeuValGlnLeuTyrlAlaValLysG 334
1001 AGGAGCCCATTTACATGTCACGAGTACATGACAGGAGGAGTTGCTG 1050
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334 LngLuproIleTyrlleValThrGlnLuproIleLysGlySerLeuLeu 350
1051 GACTTTTCAAGGGGAGACAGGCAAGTACTGCGGCTGCTCAGCTGCT 1100
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351 AspPheLeuLysGlyGlnThrGlyLysTyrcysLeuArgLeuProGlnLeuVa 367
1101 GGAATGCTGCTGAGTACGCTTCCAGGATGCGCTAGTGGAGGAGTGA 1150
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Db 361 CAAGACATTAATATTACCCCTGATCTGAGGGCAGCAAACTGCTGGTATCAGAACTTTG 420
 Qy 1204 gtgtcgaagaatgagccgagctttggcgctgctcggtctcattgaagaacaatgagtacagcg 1263
 Db 421 TTGTGCAAAATAGACAGACTTTTGGGCTGGGCCGAGTGATATGAGAGACAGCAGATATCTGCC 480
 Qy 1264 cggcgaagtgccaatattccccatcaagtgtgaacgagctccgaagctgacctctatgcccgc 1322
 Db 481 AGGGAAAGTACCAAAATTTCCCATCAAGATGAGACATCCCTGGAGGCTGCCAATATATGCTCT 540
 Qy 1324 ttccacccaagttggagcagtggtgtctctcctggagatcctctgacatgagctacccaaga 1383
 Db 541 TTTTCTATCAGATCAGATGATATGATGATCTTTGGTGATTTCTTACTATGAATAATTAACATAT 600
 Qy 1384 ggaacgggtgcacctacccctggagatggtgaacccgagagtgctgagacaagttgagcggggc 1443
 Db 601 GGGAGGACCTCATATATCCAGGTATGTCCAACTCGAGAGGTATATACAGCCCTTGAGCGTGT 660
 Qy 1444 taccgagatgccctgcccgcgcgcgagtgctcccgagctccctgcaagacctatgtgcagtg 1503
 Db 661 TATGCGATGCGGTGTCCACAGCACTGTGCAAAAAGACTTACAGCATCATGTCTCCAGGT 720
 Db 1504 tggcgaagagagagccttgagagcgagccacacttgagttacgtcaagccttctctgagag 1563
 Db 721 TGCGACAGGACCCCTGAGCAACGCCAAGCTTTGAATATTTACAGAGCATCTTAGAGGAC 780

RESULT 14
 US-09-228-603A-7
 Sequence 7, Application US/09228603A
 Patent No. 6291651
 GENERAL INFORMATION:
 APPLICANT: Hemmati-Brivanlou, Ali
 APPLICANT: Weinstein, Daniel C.
 TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF
 TITLE OF INVENTION: USE THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue, 4th Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/228,603A
 FILING DATE: 12-JAN-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-217 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 780 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..780
 US-09-228-603A-7

Query Match 21.2%; Score 341.6; DB 4; Length 780;
Best Local Similarity 65.8%; Pred. No. 6.4e-61;
Matches 513; Conservative 0; Mismatches 264; Indels 3; Gaps 1.

OY 787 tggagatccctcggagatcgctgsgcttggaagctcgtgcgaacgtcgtgcccaaggctcttggc 846
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Db 1 TGGGAGATCCCGCGGGAATCACTGACTGCAGAGAAGAGCTTGGACGTTCGACAGTTTGGG 60
OY 847 gaggttgagatvggagacctggaaacgylaccacaagggttggccataaaaaaaccttgaagc 906
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Db 61 GATGTTTGTTGGCCATGTATACAATGAGACACAAAGAATAGCTGTAAAAAATGAAAGCCA 120
OY 907 ggcagaatgcttcagaagagccttcctctgcagaaggcccagytgatataagaagttagact 966
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Db 121 GGACACATGTCGCCCGGAGTCCCTCTTAAGAGGCAAAATCTGATGAAGGCTTGACGCAAT 180
OY 967 gagaagctggagcaatttatgc---tgtgtttcaagaagagccaattacatcgtcaag 1023
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Db 181 GACCGCTGCGTCCGTTTGCAATGCCCTTGTGACTCAGGGGGGAACCAATATATCATTA 240
OY 1024 gagtaatgagcaaggaggagtttgtcttggaacttctaagggggagacaaggcaagtactgt 1083
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Db 241 GAGTATATGCAAAAAGSGCAGTTGCTGGATTTCCTGAAGAAAGTAAGTAGTGCCACAA 300
OY 1084 cgcctgcctcagctgtgttgacaatgctgcataagctcctcaagctcgaatggcgtactgtgag 1143
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Db 301 CCTCATTTAACTCATTTGACTTCTCTGCCAGATTTGCGAAGAGATGTGGTTTATTTAGG 360
OY 1144 cggaatgaactacgtccaccggagccttcgttgagccaacatcctgttggaagaagaccgt 1203
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Db 361 CAAAGGAATTTATTTACCCTGATCTGAGGCGACAAATGCTGTGATACAGAACTTTG 420
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Db 421 TTGTCAAATAATGACAGACTTTGGCGCTGGCCCCAGTATGATGAGACAGCAGATATATGCG 480
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Db 481 AGGGAAGGTACCAAAATTTCCCATCAAGTGCATCCCTGAGAGCTGCCAATTATGCGTCT 540
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Db 541 TTACTATCAACTCAAGATGATGTCATTGGTGTATTTCTTAATCAATAATAAACATATAT 600
OY 1384 ggaagggtggccctaccctctggatgttgaaacgscgaagtgctgtaaccaggttgagcgggc 1443
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 601 GGGAGGACTCCATATCCAGGTAATGTCACAACTGGAGGTAATTAACAGCCCTTGAGCGTGG 660
OY 1444 taccgatgcccctgcgcgcgcgagagtgtcccgagtccctctgcagaacctatgtgcagtlgc 1503
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 661 TATGCATGCGCTGATCCCGACACTGTGTCAAAAAGACCTCTACAGCATGCTCCAGTGT 720
OY 1504 tggcggaaagagcctctgagagcgcggcccaccttcgagtaactctgaagcctctctcggagac 1563
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 TGGCAGCAGGACCTGAGCACAGCGCCAAAGCTTTGATATTATTACAGAGCATCTTAAGAGGAC 780

RESULT 15
US-08-426-509A-5
Sequence 5, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizky, Mikhail
APPLICANT: Sures, Imran G.
TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

```
||||| | |||| | ||||| || ||||| ||||| |||||
Db 807 TGCCTTCCTGGAAGAGCAATCTGATGAAGAGCTGCAGATGACCGGCTGCTGTT 866
Oy 984 gtagtc---tgtagtcaagagagccattacatcgtaacgagatcaatgagcaagg 1040
Db 867 GCATGCCCTTGTGTGCTAGAGGGGAAACCAATATATATCTGCTGATATGCAAAAGG 926
Oy 1041 gatttgcgtgaactcttcaagaggagagcaagtaactgcgtgcgtcctcaagctgt 1100
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Oy 1101 ggaatagctgtcaatcgccatcgatcgatcgatcgatcgatcgatcgatcgatcgat 1160
Db 987 TGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046
Oy 1161 cggagactcgtgcaacgaacacacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1220
Db 1047 CCGTGAATCTGAGGCGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
Oy 1221 ctttgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 1280
Db 1107 CTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 1166
Oy 1281 ccccatcaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1340
Db 1167 TCCCATCAATGAGGAGCATCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226
Oy 1341 cgtgtgtccttgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 1400
Db 1227 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
Oy 1401 tggagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1460
Db 1287 AGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1346
Oy 1461 gccgagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1520
Db 1347 CACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1406
Oy 1521 gggagggcccaactcgtgagtaactgcagcagcagcagcagcagcagcagcagcagc 1580
Db 1407 GCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466
Oy 1581 gcccaagtaccagcc 1595
Db 1467 AACACAGTACCAAGC 1481
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RESULT 11
US-09-173-581-12
Sequence 12, Application US/09173581A
tent No. 6013455
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GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 1574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
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OTHER INFORMATION: 507669
US-09-173-581-12
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Query Match 21.5%; Score 346.2; DB 3; Length 1574;
Best Local Similarity 70.1%; Pred. No. 8,5e-62;
Matches 465; Conservative 0; Mismatches 198; Indels 0; Gaps 0;
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Oy 933 gcaagagcccaagtcagtaagaagcagcagcagcagcagcagcagcagcagcagcagcagc 992
Db 464 gcccgagcccaactcagtaagaagcagcagcagcagcagcagcagcagcagcagcagcagc 523
Oy 993 gtttcaagagcccaactcagtaagaagcagcagcagcagcagcagcagcagcagcagcagc 1052
Db 524 gttcaccagagcccaactcagtaagaagcagcagcagcagcagcagcagcagcagcagcagc 583
Oy 1053 ctttcaagagcccaactcagtaagaagcagcagcagcagcagcagcagcagcagcagcagc 1112
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Db 644 ccaattgcagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 703
Oy 1173 tgcagcccaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1232
Db 704 ggcagcccaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 763
Oy 1233 tgcagcccaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1292
Db 764 agcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 823
Oy 1293 gacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1352
Db 824 gacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 883
Oy 1353 cggagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1412
Db 884 tggagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 943
Oy 1413 ccgagagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1472
Db 944 ccgagagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1003
Oy 1473 cgaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1532
Db 1004 agagagagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1063
Oy 1533 cttgagtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1592
Db 1064 cttgagtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1123
Oy 1593 gcc 1595
Db 1124 gcc 1126
```

```
RESULT 12
US-09-420-915-12
Sequence 12, Application US/09420915
Patent No. 6264847
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
```

QY 892 aaacccctgaagcctggcagatgtctccagagccttcctcgaagagccagctcatg 951
1067 AAAACACTAAACACGATGACATATGACAGAGCTTTCTTCAAGAGCTCAGTAATG 1126
QY 952 aagaagctgagcagtgagagcctgtgtcagttgtatgtctgtgttcagagagccatt 1011
1127 AAAAATAAGACATGATGTAACCTGTTCCACTATATGCTGTGTTCTGAAGAGCAATT 1186
QY 1012 taactgctacgaggtatcatgagcaagggggtttgtcgtgaccttctcaaggggagaca 1071
1187 TACATTGTCACTGAATGATGATCAAAAGAGCTTATTCATTCTTCAAGAGAGAT 1246
QY 1072 gcaagatcctgctgctgctcagctggtgtgacgtgtgtcctcaagctcagcagctg 1131
1247 GGAAGATTTTGAAGCTTCCCAAAATGTTATGCTGCTCAATTTGCTGATGATG 1306
QY 1132 gcgtacgtgagcagatgaatcagctcaccgagacctctgtcagcaacaatcctgtg 1191
1307 GCATATATTAAGAAAGAACTATATTCACCGAGATCTCTGGGCTGCTAATATCTTGT 1366
QY 1192 gaggagaaactgtgtgtcgaagtgccagcttgggtgtgtgtcgtcgtcattgagacaat 1251
1367 GGAGAAATCTTCTGTCAAAATAGCAGATTTGTTAGCAAGGTATATGAAGACAT 1426
QY 1252 gagtacacgctgctgctgctgctcgaatctcccatcaagtgtgagcgtcctcagagctg 1311
1427 GAATATCATATCAACAAAGGTCAGAAATTTCCATCAATCAATGACGCTCGAATTTGCA 1486
QY 1312 cctcatgctgctcctacacatcaagctgagcgtgtgtcctcctcagagctcctgtcag 1371
1487 CTGATGCTGGGTTTACAAATGCTGTGCTGCTCATTTTGAATCTTCAAGACAA 1546
QY 1372 ctcaaccaaaggagcgggtgctcctcctcctcctcctcctcctcctcctcctcctc 1431
1547 CTGTAAACAAAGGTCAGAGTCCATATCCAGTATGGAACCAATGATCTGGAACAG 1606
QY 1432 gtgagaggggctcagcagctgctgctgctgctgctgctgctgctgctgctgctg 1491
1607 GTGAGGAGAGATACAGAGTCCCTGCTCAGGAGCTGTCCAGAAATCCCTCATGAAATG 1666
QY 1492 atgtccagctgtcgtcgaagcctgagagcgtgagcgtcctcagcttctacgtcagc 1551
1667 ATGATGTGTGTTGAGAGAGACCTGATGATAAAGCAATTTGATATGATGATGCTC 1726
QY 1552 tctcctgaggaactctcctcagctcagcagcagcagcagcagcagcagcagcagc 1610
1727 TTTCTTGGAGACTACTCTACCTGCTACAGAGCATATGATCCAGCAGAGAAACTTCTA 1785
Db

9-006-675-1
Patent No. 5952213
GENERAL INFORMATION:
APPLICANT: Hemmati-Brihanlou, Ali
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,675
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1491
US-09-006-675-1

Query Match 28.9%; Score 465.8; DB 2; Length 1491;
Best Local Similarity 61.6%; Pred. No. 5,2e-86;
Matches 822; Conservative 0; Mismatches 492; Indels 21; Gaps 4;

QY 264 cttgtgcccctatgactatgagctagagcagcagcagcagcagcagcagcagcagcagc 323
165 CTTGCTGCTTGTATGACTATGATGAGATCCACCTGGGAGATCTACTTTTGAAGAG 224
QY 334 cgaagcgtcctcagatctgtcaacaacagcagcagcagcagcagcagcagcagcagc 383
225 GGACCATCTCC--TGCTAAAGAAAGATCAGAGGAGGTGTTGGAAGCATGTAAATTC 281
QY 384 ccaagagacagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 443
282 CACTGCTGTAAGAGGCTTTGTTCCAGTATGATGAGTATTAATTCCTTGGAATC 341
QY 444 tgaagagtgatcttttgaagagacacagcagcagcagcagcagcagcagcagcagc 503
342 TGAAGATGCTCTTTAAAGCATGACCGGAAAGAGCTGAAGGACAGCTGCTATCTCC 401
QY 504 agagacccgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 563
402 TGTATATAAAGTGGGGCTTTCATGATCCGAGACATGAGACATGAAGTTGTTCTC 461
QY 564 cctcctcagtgctgactcagacacagcagcagcagcagcagcagcagcagcagcagc 623
462 CCTCTCTGTGCGAGACT-----CAGGGGACACTGTGTAACATTAACAAATTCG 509
QY 624 caagctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 683
510 CACACTCGATGATGAGGTTCTTCAATTTCTACAGGATCCCTTTCTCTTCTTGCCAGA 569
QY 684 gctgtgacctactcctcaaacacgagcagcagcagcagcagcagcagcagcagcagc 743
570 GCTGTAGGCACTTATCAAGATGAAGTGAATGCTGTCAAGTGTCTTCAATATACATG 629
QY 744 ccccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 803
630 CCAAACTGTGCTCCAGAGAAACCATG--GGAAAGATGCTGGAAGATTCCTCCGGCGA 686
QY 804 gtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 863
687 GTCACTGTCACTGCAAGAGAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 746
QY 864 ctgagacgtacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 923
747 GTACATATGACACAAAGATGCTGTATTAACATGAAGCCAGGAGCATGTCCCGCG 806

D	781	GATGCTGTGGAGATCCCTCGGGATCGGCTGGAGTGGAGTCAAGCTGGGGCCAGGGCTGC	840
Q	841	tttgccgagtgctgagtaggggaactctgaaaggtaccacagggctgagccatcaaaccttg	900
D	841	TTTGGCGAGGTGTGGATNGGGGAACTGGAAACGCTACCAACAGGGGTGCCATCAAAACCTTG	900
Q	901	aagccttgccagcagctgctccaggaagccttcctgtgaaggaagcccaagtcataagaaagctg	960
D	901	AAGCCTTGCCAGCAGCTGCTCCAGAGAGCCTTCCTCTGCAAGGAGCCCAAGCTCAAGAAAGCTG	960
Q	961	aggcatggaagcctgctgcaactgtatcgtctgtgtttccaagagagcccatctacatgcgc	1020
D	961	AGGCATGGAAGCTGTGTCGATCTTGTATGCTGTGGTTTCAAGAGAGCCCATTTACATCGTC	1020
Q	1021	acggaatcatatgacccaagggagatttgcctggaacttccaaagggagagacaagcgaatgac	1080
D	1021	ACGGAGTCAATGACCAAGGGGAGATTTCCTGGACTTTCTCAAGGGGGAGACAGCAAGTAC	1080
Q	1081	ctgccggcgtccctcagctcgtgtagaatagtgcctgcataagctccagtcagatgctcgtg	1140
D	1081	CTGGCGGCTGCTCTAGCTGTGTGGAATGTGGCTCTACATCCCTCCACAGCAATGGGCTACGTG	1140
Q	1141	gagcgaatgaactcgtccacacggagaccttcgtgcagccaactcctgtgtgggaaggaac	1200
D	1141	GAGCGGATGAATCTACGTCCACGGGACCTTGTGTCACCAACATCTGTGGGAGAGAAAC	1200
Q	1201	ctggctgtgcaaaagtgcgcgaactcttgagctgtgcctgcatactgaagaaatgtagtacag	1260
D	1201	CTGGGTGTCAAAAGTGGCGCACTTTGGGCTGTGGCTGCTCATTTGAACAAATAGTAGTACAG	1260
Q	1261	gcgcggcgaaggtgtccaaattcccaataagctggaacggtccagaagctgcctctatggc	1320
D	1261	GCGGGCGCAAGGTGCCAAATTCCCATCAAGTGCAGGCTCCAAACCTGGCCCTCTATGGC	1320
Q	1321	cgcttaccacaaagctcgaagcgtgtgtctcttcggagatccctgtgtgactgaatcacacaa	1380
D	1321	CGCTTACCAATCAAGTGGAGAGTGTGTTCTTGGGATCTGCTGTGATGACTGACTACACAA	1380
Q	1381	aaggagcaggtgtgccctacccttggaatgtgtgaacgcgaagtgtcttggaacaggtgagcgg	1440
D	1381	AAGGAGCAGGAGTGCCTTACCTCGGAGTGTGAACCGGAGGTGTGGACCAAGTGGAGCGG	1440
Q	1441	ggtcaccagatgacctcgtccgcgcggaagtgtcccgagtcacctgacgaactcatgtgccag	1500
D	1441	GGCTACACGGAGTCCCTCCGCGCGAGTGTCCGAGTCCCTGCACAGCACTCATGTGCCAG	1500
Q	1501	tgtcggcgaagggagccttgagggagcggcccaacttgcgaatcactgcaagccttcctcgag	1560
D	1501	TGCTGGCGGAAAGAGCTGTGAGAGACGGGCCCACTTGGAGATCACTTGAGAGGCTTCCGTGAG	1560
D	1561	gactacttcacgtccacccgagcccaatcacagcccgaggagaaactctgag 1611	
	1561	GACTACTTCACGTCACCCAGGCCCAATCACAGCCCGAGGAGAACTCTGAG 1611	
RESULT 3			
US-07-820-011A-1			
Sequence 1, Application US/07820011A			
Patent No. 533615			
GENERAL INFORMATION:			
APPLICANT: Bell, Leonard			
APPLICANT: Madril, Joseph A.			
APPLICANT: Warren, Stephen L.			
APPLICANT: Lubliner, Daniel J.			
TITLE OF INVENTION: Genetically Engineered			
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced			
TITLE OF INVENTION: Migration			
NUMBER OF SEQUENCES: 4			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Maurice M. Klee			
STREET: 1951 Burr Street			

CITY : Fairfield
STATE : Connecticut
COUNTRY : USA
ZIP : 06430

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER : IBM PC XT
OPERATING SYSTEM : PC-DOS/MS-DOS 2.10
SOFTWARE : Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER : US/07/820, 011A
FILING DATE : 19920106
CLASSIFICATION : 435

AUTHOR/AGENT INFORMATION:
NAME : Klee, Maurice M.
REGISTRATION NUMBER : 30,399
REFERENCE/DOCKET NUMBER : LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE : (203) 255 1400
TELEFAX : (203) 254 1101
INFORMATION FOR SEQ ID NO : 1:
SEQUENCE CHARACTERISTICS:
LENGTH : 1602 base pairs
TYPE : NUCLEIC ACID
STRANDEDNESS : Double
TOPOLOGY : Linear
MOLECULE TYPE : cDNA to mRNA
HYPOTHETICAL : No
ANTI -SENSE : No
ORIGINAL SOURCE :
ORGANISM : Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS : Takeya, Tatsuo
TITLES : Structure and Sequence of the
TITLE : Cellular Gene Homologous to the RSV src
TITLE : Gene and the Mechanism for Generating the
JOURNAL : Cell
VOLUME : 32
PAGES : 881-890
DATE : March, 1983

US-07-820-011A-1

Query Match 75.5% ; Score 1216.6; DB 1; Length 1602;
Best Local Similarity 85.2% ; Pred. No. 5.9e-238;
Matches 1373; Conservative 0; Mismatches 229; Indels 9; Gaps 1.

Y 1 atgggtatgcaacaagaagacccaaagtatgcaggccaaggcgagcgaactgtgaagccc 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGGGAGACCAACAAGACGAAGCCCAAAGACCACGCCAGCGCGGCAGCTTGAGCCA 60

Y 61 gccagaaagctcacagcgcgctctgcygggygcctttccccgccttcagaccaccaaacaa 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CCCGACAGCACCCACAC-----GGGGATTCCACAGCTTCACAGCCCCAACAAAG 111

Y 121 ccagacctcgcgcgcgcgcacacgcgcgcgcccaagcgcgccttgcgcccccgcgccgcgag 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 112 ACACAGACGCCCCGACAGCACATCCCACGCCGCGCTTTGGAGACGTGGCCACCGAG 171

Y 181 cccaagctgttcaggagagcttaacctcctcgcagacacgcttacacctcccgccagagggcgag 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 CCGAAGCTCTTGCGGGGGCTTAACAACATTCTGACACACCGTTACTGCTCCCGACGCTCCGG 231

Y 241 ccgcttgcccggttgagtagtaccaccttctgtgcccctctaagactabagtltagagcggag 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 GCACGTGGCTGGCGCGCTACACCATTTGCTGAGCTCTACGACTACGAGTCCCGGACTGAA 291

Y 301 acagacctgttccttcaaagaagcgagcgagcgctcagatatgttcaacaacaagagagygagac 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 ACGGACTGTGCTCTCAAGAAGAAGAAAGCGCTGGAGATTGTCACACACGGAAGAGTAGC 351

XX Hanson V, Levy FO, Mustelin T, Skalhogg BS, Sundvold V, Tasken K;
PI Vang T, Altman A, Munshi A;
XX WPI: 2000-066801/07.
DR P-PSDB: AAY49420.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative
PT disorders, e.g. cancers or autoimmune diseases
XX
PS Claim 22: Page 94-95; 11pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV
CC infection, AIDS, common variable immunodeficiency or cancers. Conditions
CC in which upregulation of the PKA pathway is required, such as autoimmune
CC disease, e.g. systemic lupus erythematosus, may also be treated. The
CC present sequence represents a DNA sequence encoding a PKA substrate,
CC wherein the substrate is in the Src-family, preferably Lck, Fyn, Src,
CC Yes, Fgr, Lyn, Hck Blk, Yrk, c-Kit, Fyk, Src-1 or Src-2.
XX
SO Sequence 2032 BP: 450 A; 576 C; 584 G; 422 T; 0 other;

Query Match 35.7%; Score 574.8; DB 21; Length 2032;
Best Local Similarity 65.6%; Pred. No. 2e-99;
Matches 872; Conservative 0; Mismatches 452; Indels 6; Gaps 2;

QY 266 ttgtgagcctctatgactatgagtagagcagagagcagcttccaaagaagcg 325
DB ttatgctcttcacagcagcagcctctcaacgagatccttgagaaaggag 307
QY 326 agcgcctcagatgtcaacaacagcagagagctgctgctgcccactgcctaga 385
DB aacctctcgatcctctgagca---gagcgagagtggtgagagcgccatccctgaca 364
QY 386 cagcagcagcagctacatcccccagcagcagctgctgctcctcagctccagctg 445
DB cgagcagcagcagctcctcctccatcttctgtgcaaaagcagcagcctgagccg 424
QY 446 agcagtgatatttgcaagatcacacagcagcagctgctgagcgttaccgtcaatgcag 505
DB aacctgtctctcaagaacgctgagcagcagcagcagcagcagcagcctccgagccg 484
QY 506 agaacccagagagcactcctcctgctgagagagtgagcagcagagtgctctatgc 565
DB ggaacacccagcagcctcctccatccatccagagagcagcagcagcagcagcagcagc 544
QY 566 tctcagtgctgacttgcaacagcagcagcagcagcagcagcagcagcagcagcagc 625
DB tctcagtgctgacttgcaacagcagcagcagcagcagcagcagcagcagcagcagc 604
QY 626 agctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 685
DB atctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 664
QY 686 tgggtgctactacccaacacagcagcagcagcagcagcagcagcagcagcagcagc 745
DB tgggtgctactacccaacacagcagcagcagcagcagcagcagcagcagcagcagc 724
QY 746 caacgtccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 805
DB agaccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 781

QY 806 cgcctcgcgtgaggtcaagctggtgcccagcagcagcagcagcagcagcagcagcagc 865
DB cgcgtgagcgtggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 841
QY 866 ggaacggtacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 925
DB acaacggtacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 901
QY 926 ccttcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 985
DB ccttcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 961
QY 986 atgctgtggttcacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1045
DB agcgtgtggttcacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1021
QY 1046 tgcctgacttctcaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1105
DB tgcctgacttctcaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1081
QY 1106 tggctctcagatcgctcagcagcagcagcagcagcagcagcagcagcagcagcagc 1165
DB tggctctcagatcgctcagcagcagcagcagcagcagcagcagcagcagcagcagc 1141
QY 1166 acctcgttcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1225
DB acctcgttcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1201
QY 1226 ggcctgctcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1285
DB ggcctgctcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1261
QY 1286 tcaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1345
DB tcaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1321
QY 1346 ggtccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1405
DB ggtccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1381
QY 1406 tggtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1465
DB tggtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1441
QY 1466 agtgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1525
DB agtgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1501
QY 1526 ggcacaccttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1585
DB ggcacaccttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1561
QY 1586 agtacacagc 1595.
DB agtacacagc 1571

RESULT 13
AAT71262
ID AAT71262 standard; DNA; 1804 BP.
XX
AC AAT71262;
XX
DT 30-MAR-1998 (first entry)
XX
DE Human c-yes-2 gene.
XX
KW Cognate transgene; human; c-yes-2; lymphoma; cellular immunogen; cancer;
KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
KW colon carcinoma; immunotherapy; proto-oncogene; ss.
XX
OS Homo sapiens.
XX

Sequence 4517 BP; 1437 A; 784 C; 955 G; 1341 T; 0 other:

```
Query Match      44.1%; Score 710.2; DB 22; Length 4517;
Best Local Similarity 70.1%; Pred. No. 6.9e-125;
Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

OY 248 ccggtgagtgagacacacctgtgtgcccctcctacgtactgtatgtatgacgaggaagacac 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 476 caggtgtgttactatattgtgtgcccctcctacgtactgtatgtatgacgaggaagacac 535
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 308 tgccttcaagaagagcgagcgagcctcagattgttcaacaacacgaggaagagcggtgtgac 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 536 ttccatttaagaagagcgaggaagattcaataataaacaagaagagaggtgtgtgg 595
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 368 tggcccaactgcgtcagacagaggaagacagagctacatcccaagaactactgtgtgcctc 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 596 aagcaagatcaatccgctacaggaagatgttataatccgagcaactatgtacgcgcctg 655
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 428 ccgactccatccagagcggtgagaggtgtattttgcaagatccagacgcgaggtcagagac 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 656 cagattccattcagcgaggaagatgtattttgcaaaaatggggaggaagaagatgtctgaa 715
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 488 ggttactgtcctaattgcagagaacccgagaggaaccttcctctgtgcgagaagtgaagaca 547
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 716 gattactttgataatcccggaatcaacgaggtattttccttaagaagagaggtgaagaa 775
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 548 cgaaggtgctactactgcctcctcagtgctgtgactcgaacacgacgaggtccctcaactga 607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 776 ctaaggtgttattccctctcctctcctatcgtgtgtgtgtgataagaggtgtacatgtga 835
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 608 agcactacaagaatcccggaagctgagcgagcggtcttataacacgcccgcgcacagt 667
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 836 aacactcaaaaatcagaagaacttgacaatgtgtgataataatacaacacgagagacacat 895
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 668 tcaacagcctgcagcagcagctgtgtgctactactcaacaacgcgaggtgctgtgcaccc 727
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 896 ttgatactcgcagaatattgtgaacactacacagaaacatgcgtgtgttatgtccaca 955
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 728 gctcaccacacgtgtgcccacagctcccaagcgacgagactcagggcctgtgcagagatgct 787
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 956 agtgcacaactgtgtgtcctcaactgtgaaaacctcagactcaaggtctagaacaaagatgct 1015
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 788 gggagatccctcggaggtgtgctgctgctgaggtgcaggtgagcgaggtgctgtgcg 847
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1016 gggaaatcccccggagaaactcttcgcagactagaggttaaaactggaacagagatctgcgcg 1075
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 848 aggtgtgagtgaggaacctgtgaacgttaacacacagaggtgtgcacataaaccttgaagctg 907
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1076 aaggtgtgagtgaggaacctgtgaacgttaacacacagaggtgtgcacataaaccttgaagctg 1135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 908 gcacgatgtctcagagagcctctcgtcagagagccaggtcatgaaagagctgtgacatg 967
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1136 gtacaatgatcgcagaagcttctcctcctcaagaagctcagataatgaaaaataagaacatg 1195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 968 agaaagctgtgagcattgttatgtgtgttcaaggagcccatatactgtcagagaggt 1027
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1196 ataactgttccacataatgtcgtgttcttgaagaacacattacatgtgcactgagat 1255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1028 acatgagcaagggaggttctgtgacttcccaaggggaggaacagcagcagactccgcgcg 1087
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1256 ttatgtcaaaaagagctatagattccttaagaagagagatgtgaagatatttgaagc 1315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1088 tgcctcagctgtgtgaacatgctcctcagatcgcctcagacatggcgtgacgtgagcgga 1147
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1316 ttccacagctgtgtgatattgtctcagattgtcgtatgtgacataatataagaagaa 1375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1148 tgaactacgtccacggagacttctgtgacgcaaatcctctgtgtgagagaacgtgtgt 1207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1376 tgaactatattcaccgagatctcgtgtcctaattcttctgtagagaaaactctgtgt 1435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1208 gcaaggtgcgagacttgcgtgtgctgcacatgaaacacatagatacagggcgcg 1267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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```
DB 1436 gcaaaaatagcagacttggtttagcaggttaattgaagacaatgaataacacagcaagac 1495
OY 1268 aaggtgccaaattccccaagtggagcgctccgaagacgtgcctctatgtgcgcctca 1327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1496 aaggtgccaaattccccaagtggagcgctccgaagacgtgcctctatgtgtgtgtg 1555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1328 ccatcattcggagcgtgtgtgtccttcggatcctgtcgtactgtgagctcaccacaaggagc 1387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1556 caataaagctcgtatgtcgtcatttggatattctcgaacagaactagtaacaaggagcc 1615
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1388 ggtgtgcctaccctggatgtgtgaacccgaggtgtcgtgacagaggtgtgagcggtacc 1447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1616 ggtgtgcctaccctggatgtgtgaacccgaggtgtcgtgacagaggtgtgagcggtacc 1675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1448 ggtgtgcctaccctggatgtgtgaacccgaggtgtcgtgacagaggtgtgagcggtacc 1507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1676 ggtgtgcctaccctggatgtgtgaacccgaggtgtcgtgacagaggtgtgagcggtacc 1735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1508 ggaaggaacctgagagagcgagcgacacactcgaatcgtcgaagcctcctcgtgagactact 1567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1736 agaaggaacctgagagagcgagcgacacactcgaatcgtcgaatcgtcgtgtgtgga 1795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1568 tcaagtcacacgagcccgatcaccagcccggtgagaaacctcta 1610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1796 tcaagtcacacgagcccgatcaccagcccggtgagaaacctcta 1838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
AAS74489
ID AAS74489 standard; cDNM: 4517 BP.
XX
AC AAS74489;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #10293.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX P-PSDB: ABG10302.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID NO 10293; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
```


RESULT		7
AAH18556		
ID	AAH18556	standard; cDNA; 3299 BP.
XX		

AC AAH18556;
XX 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:18723.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
XX EPI074617-A2.
XX
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99UP-0248036.
XX 27-AUG-1999; 99UP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES. INSTR.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX
PS Claim 8; SEQ ID 18723; 2537/PP + CD ROM; English.
XX
XX
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 3299 BP; 604 A; 981 C; 996 G; 718 T; 0 other;

Query Match 56.4%; Score 908; DB 22; Length 3299;
Best Local Similarity 98.9%; Pred. No. 3,8e-162;
Matches 914; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

688 gtggctactactccaacacgcgcgatgctgtgcccacgcctccacacgctgtggccc 747
DB ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
334 ggggctgtcgcgtcgggaacacgcgcgatgtgctgtgcccacgcctccacacgctgtggccc 393
DB ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
748 acgtccaaagccgcgactcaaggcctgtgccaagatgctgtggaatccctcggagctcg 807
DB ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
394 acgtccaaagccgcgactcaaggcctgtgccaagatgctgtggaatccctcggagctcg 453
DB ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |

[illegible]

PM W09314193-A.
PD 22-JUL-1993.
XX
XX 05-JAN-1993; 93WO-US000445.
XX
XX 06-JAN-1992; 92US-0820011.
XX
XX (UYTA) UNIV YALE.
PA
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
PI WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
XX Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn
PT
XX
XX Disclosure; Page 59-62; 91pp; English.
PS
XX The DNA encoding a portion or (more preferably) the entire pp60
CC c-src polypeptide is used to transform endothelial cells.
CC
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than
CC non-transformed counterparts; have an enhanced ability to inhibit
CC the formation of thrombi and/or dissolve thrombi once they have
CC formed and exhibit reduced mononuclear cell adhesion. They can al
CC be used to improve the success of surgical procedures such as
CC coronary angioplasty, heart bypass surgery, vessel graft and stent
CC implantation.
CC
SQ Sequence 1602 BP; 350 A; 503 C; 481 G; 268 T; 0 other;

Query Match	Similarity	75.5%	Score 1216.6	DB 14	Length 1602
Best Local	Similarity	85.2%	Pred. NO. 2.7e-220		
Matches 1173	Conservative	0	Mismatches 225	Indels 9	Gaps 1
QY	1 atgggttagcaaaagacagacagcccaagagatgacagccacagcgcgccgcgcgcacgctctggagccc	60			
DB	1 atggggagagagaagaagagacagcccaagagacccacgacagcgcgcgccgcgcacgctctggagcca	60			
QY	61 gccggagaaagctcgaagcgctggcgggcgcttcccgcgctctgcagaccccccagaag	120			
DB	61 cccggacagacccacacacac-----ggggattcccaagcctctgcagaccccccacaag	111			
QY	121 ccagcctcggccgaagcgccacgcggccccaagcgcgctctgcgcgcccgcgccgcag	180			
DB	112 aagacgaccccccgacagacgacgcacccccacgcgctcctcttggagacgctggccacag	171			
QY	181 cccaagctgtctcgagagcttcaactcctctcgaaacacgctcaactcccgacagagcgggc	240			
DB	172 cccaagctctcttggggctctcaacactcttcgacacacggtacgctgcgcgagcgctgcggg	231			
QY	241 ccgcctggccgggtggaggttgacacactttggcgccctatgactagatgactgagagcgggg	300			
DB	232 gcaatgacggcgggcgctccacacttctcggtctctctcaagactcaagatcccggaatgaa	291			
QY	301 acaagacctgtccctcaagaaagcgagcgcgctccacagattgtcaacaacaacgagagggag	360			
DB	292 acgagactgtctctcaagaaagagagacgctgcagatgtgtcaacaacaacgagaagtgac	351			
QY	361 tgggtgtctggcccaactcgtctcagacagagacacagagtgataatccccgaactacg	420			
DB	352 tgggtgtctgtccatctccctcactacagagacagaggggtataatccccgaactatgtc	411			
QY	421 ggccctccgactcaatccacagctagagagtgtaatttggcaagatcacccagacagagag	480			
DB	412 ggcgcctcagactcaatccagagctgaaagagtgtaatttgggaagatcacctgttcgggag	471			
QY	481 tcaagacggtactcgtctcaatgcagagaacccggaagaggaactctcgttcgagaaagt	540			

RESULT 3

AA229700
ID AA229700 standard; cDNA; 1759 BP.

AC AA229700;

DT 22-MAR-2000 (first entry)

DE Wild-type chicken c-Src tyrosine kinase cDNA.

XX Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
XX chicken; viral expression vector; replication competent; variant Src;
XX inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
XX diabetic retinopathy; osteoporosis; cancer; ss.

OS Gallus sp.

XX Key Location/Qualifiers

FT CDS 112..1713
FT /*tag- a
FT /product- "Chicken c-Src tyrosine kinase"
FT /note- "Src used to modulate angiogenesis"

XX MO9961590-A1.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US11780.

XX 29-MAY-1998; 98US-0087220.

XX (SCRI) SCRIPPS RES INST.

XX Chersesh DA, Elliceiri B, Schwartzberg PL;

XX WPI: 2000-116335/10.

XX P-PSDB; AAY44447.

XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism -

XX Claim 1; Fig 1; 80pp; English.

XX The present sequence is the cDNA, encoding the wild-type chicken c-Src
XX tyrosine kinase. This sequence encoding the Src protein, can be used to
XX modulate angiogenesis. When the Src protein is inactivated, angiogenesis
XX is inhibited, while when it is activated, angiogenesis is potentiated.
XX The modified or variant Src can be used to treat inflammatory diseases
XX like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
XX osteoporosis and cancer associated disorders.

XX Sequence 1759 BP; 370 A; 554 C; 533 G; 302 T; 0 other;

Query Match 75.6%; Score 1218.2; DB 21; Length 1759;
Best Local Similarity 85.3%; Pred. No. 1.4e-220;
Matches 1374; Conservative 0; Mismatches 228; Indels 9; Gaps 1;

QY 1 atgggtgcaacaagaccccaagatgacagccagcgccgacgctgtgagccc 60
DB 112 atggggagcagacagacaccccaagacccagcgccgacgctgtgagcca 171
QY 61 gccagagacgtgacgagcgctgagcgccgttcctccgctcgcagaccccgcaag 120
DB 172 ccgacagcagccacacac-----ggggattccagcctgcgacaccccccacaaag 222
QY 121 ccagcctgcgacgagccagcgccgagcgcccttcgcccgcgagcgcgag 180
DB 223 acagcagcccgacagcagcagcagcccgacgctccttggagacgtgacagcgag 282
QY 181 ccaagctgttcgagagcttaactcctcggacacgctcaactcccgacagagggcgagc 240

DB 283 cccaagctcttcgggggttcacacactctctgacacggttgcgcgagcgctgcggg 342
QY 241 ccgctgcgcggtgagtgacacacacttctgctgacctctatgactatgactagagcgag 300
DB 343 gcaactgctgcgagcgctacacacttctgctgacctctatgactagagcgagcgagcgag 402
QY 301 acagacctgtctctcaagaagaagcgagcgctccagatctgtcaacaacgagagagac 360
DB 403 acgagactgtctctcaagaagaagcgagcgctccagatctgtcaacaacgagagagac 462
QY 361 tgggtgctgcgacactctgcagcagcagcagcagcagcagcagcagcagcagcagcag 420
DB 463 tgggtgctgcgacactctgcagcagcagcagcagcagcagcagcagcagcagcagcag 522
QY 421 ggcacctccagactccatccagcagcagcagcagcagcagcagcagcagcagcagcag 480
DB 523 ggcacctccagactccatccagcagcagcagcagcagcagcagcagcagcagcagcag 582
QY 481 tcaagagcggttaactctcaatgacagagaccccgagagagcctctctgtgcgagaaat 540
DB 583 tccgagcggtgtgtctcaaccccgagagaccccgagagaccccgagagaccccgagagac 642
QY 541 gagaccacgaaaggtgctcactgctctcagtgctgacttgcagacacgacgagcgctc 600
DB 643 gagaccacgaaaggtgctcactgctctcagtgctgacttgcagacacgacgagcgctc 702
QY 601 aacgtgaagcactacacagaccccgagagcagcagcagcagcagcagcagcagcagcag 660
DB 703 aatgtgaagcactacacagaccccgagagcagcagcagcagcagcagcagcagcagcag 762
QY 661 accagatcaacagcctgcagcagcagcagcagcagcagcagcagcagcagcagcagcag 720
DB 763 acacagttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 822
QY 721 tgcacccgctcaccacgctgtgcacacgcttcagcagcagcagcagcagcagcagcag 780
DB 823 tgcacccgctcaccacgctgtgcacacgcttcagcagcagcagcagcagcagcagcag 882
QY 781 gatgcttgagagatccctcgtgcagcagcagcagcagcagcagcagcagcagcagcagc 840
DB 883 gacggtgtggaatcccccggagctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 942
QY 841 ttgtgcagaggtgtgagtgagcctgcagcagcagcagcagcagcagcagcagcagcagc 900
DB 943 ttgtgcagaggtgtgagtgagcctgcagcagcagcagcagcagcagcagcagcagcagc 1002
QY 901 aagctgcagcagcttcccaagcagcagcagcagcagcagcagcagcagcagcagcagc 960
DB 1003 aagctgcagcagcttcccaagcagcagcagcagcagcagcagcagcagcagcagcagc 1062
QY 961 aggcattgagagcgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagc 1020
DB 1063 cggcattgagagcgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagc 1122
QY 1021 accgagttacatgacgagagagagctgtgcagcagcagcagcagcagcagcagcagcag 1080
DB 1123 actgagttacatgacgagagagagctgtgcagcagcagcagcagcagcagcagcagcag 1182
QY 1081 ctgcgagctgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1140
DB 1183 ctgcgagctgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1242
QY 1141 gagcagatgaactacgtccacgagcagcagcagcagcagcagcagcagcagcagcagcag 1200
DB 1243 gagcagatgaactacgtccacgagcagcagcagcagcagcagcagcagcagcagcagc 1302
QY 1201 ctgtgtgcacaaagtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagc 1260
DB 1303 ctgtgtgcacaaagtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagc 1362
QY 1261 ggcgagcagaggtgtgcacaaattcccatcagagtgagcagcagcagcagcagcagcagc 1320

401 ACATCCCAAGAACTAGCTGGCGCCCTCCGACTCCATCCAGGCTGAGAG 450
|||||
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501 TGCAGAGAACCCGAGAGGACCTCTCTGTCGAGAAAGTGAGACACAGA 550
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551 AAGTGCCCTACCTGCTCAGTGTCTGACTTCGACACAGCCAGGCGCTC 600
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601 AACGTGAAGCACTACAGATCCGCAAGCTGGACAGCGCGCTTACAT 650
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198 AsnValLysHisTyrlaArgIuLysLeuAspSerGlyGlyPheTyrl 214
651 CACCTCCCGACCCAGTTCACAGACCTGACAGCTGGTGCGCTTACT 700
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214 eThSerArgThrGlnPheSerSerleuGlnGlnValaIaTyrlTyrS 231
701 CCAAAACAGCCGATGCGCTGTGCCACCGCTCACCCAGCTGTGCCACG 750
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231 erLysHisAlaAspGlyLeuCySHisArgLeuThrAsnValCysProthr 247
751 TCCAGCCGCACTCAGAGCGCTGGCCCAAGATGCTGGAGATCCCTCG 800
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901 AAGCTGGCAGATGTCTCCAGAGGCTTCTCTGAGAGGCCAGGTCAT 950
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298 LysProGlyThrMetSerProGlnAlaPheLeuGlnGlnAlaGlnValMe 314
951 GAAGAAGCTGAGCATGAGAGCTGTCATGTCATGTCGTTGAG 1000
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: GENERAL INFORMATION:
: APPLICANT: Bell, Leonard
: APPLICANT: Madri, Joseph A.
: APPLICANT: Warren, Stephen L.
: APPLICANT: Luthinger, Daniel J.
: TITLE OF INVENTION: Genetically Engineered
: TITLE OF INVENTION: Endothelial Cells
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESS: Maurice M. Klee
: STREET: 1951 Burr Street
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 760 Kb storage
: COMPUTER: DELL 486/50
: OPERATING SYSTEM: DOS 5.0
: SOFTWARE: Displaywrite 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00445
: FILING DATE: 19930105
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/820,011
: FILING DATE: 06-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: ALX-101PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 255 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 533 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: Linear
: MOLECULE TYPE: Protein
: HYPOTHETICAL: NO
: FRAGMENT TYPE: Complete Sequence

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documentation_block:
ID AAY29668 standard; Protein: 496 AA.
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AC AAY29668:
XX
DT 03-NOV-1999 (first entry)
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DE Human src-family kinase laloo protein.
XX
KM Human; laloo; src family kinase; SFK; proto-oncogene; gene therapy;
XX developmental disorder; tumour formation; genetic vaccine.
XX
OS Homo sapiens.
XX
PN US952213-A.
XX
PD 14-SEP-1999.
XX
PF 13-JAN-1998; 98US-0006675.
XX
PR 13-JAN-1998; 98US-0006675.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Hemmati-BriVanlou A, Weinstein DC;
XX
DR WPI: 1999-527015/44.
N-PSDB; AA208792.

lyr Isolated nucleic acids encoding vertebrate src-family kinases useful
pr for the detection of proto-oncogenes and for diagnosing early
pr developmental defects in embryos
XX
PS Claim 22; Fig 1C; 42pp; English.
XX
CC The present sequence represents a human src family kinase (SFK)
CC designated laloo. laloo plays a key role in the transformation of early
CC stage embryonic cells to mesodermal cells and is likely to be a
CC proto-oncogene. SFK nucleic acids may be used to produce SFK proteins
CC and the functional domains of SFK, according to standard recombinant DNA
CC methodologies. The laloo SFK protein is involved in the transformation
CC of early stage embryonic cells into mesodermal cells and consequently
CC mutations its nucleic acids are major causes of early developmental
CC disorders. SFK is also thought to be a proto-oncogene involved in tumour
CC formation. Therefore, the nucleic acids may be used to study the
CC physiological and biochemical processes that cause early developmental
CC defects and tumour growth. The nucleic acids may be used as probe to
CC identify similar nucleic acids in biological samples and to quantify
CC levels of expression. They may also be used to detect alterations within
CC those nucleic acids which may be related to disease. They may also be

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CC used as primers in PCR to amplify and detect sequences encoding SFK.
CC Additionally, the nucleic acids may be used in gene therapy protocols
CC either as a genetic vaccine or as a transgene which is inserted into a
CC patients genome to rectify inappropriate, or low levels of, SFK
CC expression in the patient. The SFK proteins encoded by the nucleic acids
CC may be used to assay for agents which modulate SFK expression and
CC activity or as antigens in the production of antibodies against SFK. The
CC proteins may also be administered to a patient to rectify inappropriate,
CC or low levels of, SFK expression in a patient.
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Sequence 496 AA;

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Quality: 1441.00 Length: 538
Ratio: 3.549 Gaps: 10
Percent Similarity: 75.465 Percent Identity: 52.974

alignment_block:
US-09-444-711-1 x AAY29668 ..

Align seg 1/1. to: AAY29668 from: 1 to: 496

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15 rleuGlyPro..... 18
101 CCTCGAGAGACCCCGACAGCCAGCCTCGCGCGAGCGCCAC.....CGC 144
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283 TATGACTCTAGAGAGAGAGACAGACAGCTGCTCTCAAGAAAGCGAGCGCT 332
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333 CCAGATTGTCAACACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 382
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433 TCCATCCAGAGCTGAGAGAGGTATTTGGCAGATACACAGAGCGAGTCC 482
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483 AGAGCGGTACTGCTCAATGACAGAGAACCGGAGAGAGAGAGAGAGAGAG 532
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